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OM protein - protein search, using sw model

Run on: July 1, 2004, 13:44:42 ; Search time 16.5 Seconds
(without alignments)
1339.146 Million cell updates/sec

Title: US-10-091-085-3
Perfect score: 2250
Sequence: 1 MATSWGTVFPMVVCVCSA.....ETGVALGATFHLLQSLGISH 428

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgm2_6/ptodata/2/iaa/5A.COMB.pep.*
- 2: /cgm2_6/ptodata/2/iaa/5B.COMB.pep.*
- 3: /cgm2_6/ptodata/2/iaa/6B.COMB.pep.*
- 4: /cgm2_6/ptodata/2/iaa/6B.COMB.pep.*
- 5: /cgm2_6/ptodata/2/iaa/6B.COMB.pep.*
- 6: /cgm2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2250	100.0	428	US-09-608-285A-3	Sequence 3, Appli
2	2250	100.0	428	US-09-608-285A-5	Sequence 5, Appli
3	2250	100.0	428	US-09-240-639-6	Sequence 6, Appli
4	2250	100.0	428	US-09-240-639-9	Sequence 9, Appli
5	2250	100.0	428	US-09-350-836B-3	Sequence 3, Appli
6	2250	100.0	428	US-09-350-836B-5	Sequence 5, Appli
7	2250	100.0	428	US-09-370-285-3	Sequence 3, Appli
8	2250	100.0	428	US-09-370-285-5	Sequence 5, Appli
9	2250	100.0	428	US-09-557-800C-3	Sequence 3, Appli
10	2250	100.0	428	US-09-557-800C-5	Sequence 5, Appli
11	2250	100.0	428	US-09-370-625A-3	Sequence 3, Appli
12	2250	100.0	428	US-09-370-625A-5	Sequence 5, Appli
13	2235	99.3	428	US-09-608-285A-7	Sequence 7, Appli
14	2235	99.3	428	US-09-350-836B-7	Sequence 7, Appli
15	2235	99.3	428	US-09-370-285-7	Sequence 7, Appli
16	2235	99.3	428	US-09-557-800C-7	Sequence 7, Appli
17	2235	99.3	428	US-09-370-625A-7	Sequence 7, Appli
18	2104	93.5	405	US-09-608-285A-25	Sequence 25, Appl
19	2104	93.5	405	US-09-370-265-25	Sequence 25, Appl
20	2104	93.5	405	US-09-557-800C-25	Sequence 25, Appl
21	2104	93.5	405	US-09-370-625A-25	Sequence 25, Appl
22	1837.5	81.7	465	US-09-557-800C-56	Sequence 56, Appl
23	1837.5	81.7	465	US-09-370-625A-39	Sequence 39, Appl
24	1832.5	81.4	465	US-09-240-639-8	Sequence 8, Appli
25	999	44.4	456	US-09-240-639-2	Sequence 2, Appli
26	999	44.4	484	US-09-608-285A-27	Sequence 27, Appl
27	999	44.4	484	US-09-370-265-27	Sequence 27, Appl

28	999	44.4	484	4	US-09-557-800C-27	Sequence 27, Appl
29	999	44.4	484	4	US-09-370-625A-27	Sequence 27, Appl
30	819.5	36.4	471	4	US-09-608-285A-60	Sequence 60, Appl
31	507.5	22.6	459	4	US-09-129-112-9	Sequence 9, Appli
32	503.5	22.4	467	4	US-09-129-112-19	Sequence 19, Appl
33	498	22.1	462	4	US-09-129-112-2	Sequence 2, Appli
34	491.5	21.8	462	4	US-09-129-112-15	Sequence 15, Appl
35	489	21.7	455	4	US-09-240-639-10	Sequence 10, Appl
36	467.5	20.8	473	4	US-09-240-639-12	Sequence 12, Appl
37	446.5	19.8	454	4	US-09-240-639-11	Sequence 11, Appl
38	351	15.6	502	4	US-09-557-800C-55	Sequence 55, Appl
39	351	15.6	502	4	US-09-370-625A-38	Sequence 38, Appl
40	351	15.6	510	3	US-08-930-921-1	Sequence 1, Appli
41	347.5	15.4	529	4	US-09-240-639-4	Sequence 4, Appli
42	234	10.4	148	4	US-09-240-639-17	Sequence 17, Appl
43	186	8.3	153	4	US-09-240-639-13	Sequence 13, Appl
44	180.5	8.0	150	4	US-09-240-639-16	Sequence 16, Appl
45	179	8.0	153	4	US-09-240-639-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-09-608-285A-3
; Sequence 3, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-608-285A-3

Query Match 100.0%; Score 2250; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 6.4e-248;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MATSWGTVFPMVVCVCSAVSHRNQQTWTFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
Cy 61 RIHYTFVQKMPQQLPILEGVEFDSVVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120

Db

61

RIHVYTFVQKMPGQLPILGEVFDVSVKPGLSAFVDPQKGAETVQGLLEVAKDSIPRSHW

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Qy

121

KKTPVVLKATAGLRLLPEHKAALLFEVKEIIPKSPFLVPKGSVINDGDEGLAWVTV

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Db

121

KKTPVVLKATAGLRLLPEHKAALLFEVKEIIPKSPFLVPKGSVINDGDEGLAWVTV

180

Qy

181

NFLTQGLHGHROETVGTLDLGASTQITFLPQFEXTLEOTPRGYLTSEFMFNSTYKLYTH

240

Db

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240

Qy

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300

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241

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Qy

301

EPCYAEVLRVVRGKHLQHPVEVQSGFYAFSYYYDRAVDTMDIDYKGGILKVEDPERKAR

360

Db

301

EPCYAEVLRVVRGKHLQHPVEVQSGFYAFSYYYDRAVDTMDIDYKGGILKVEDPERKAR

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Qy

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EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKNNIETGALGATPHL

420

Db

361

EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKNNIETGALGATPHL

420

Qy

421

LQSLGISH 428

Db

421

LQSLGISH 428

RESULT 2

US-09-608-285A-5

Sequence 5, Application US/09608285A

Patent No. 6335013

GENERAL INFORMATION:

APPLICANT: Ford, John

APPLICANT: Mulero, Julio

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE

TITLE OF INVENTION: POLYPEPTIDES

FILE REFERENCE: 28110/36570

CURRENT APPLICATION NUMBER: US/09/608,285A

CURRENT FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: 09/583,231

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 09/557,800

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: 09/481,238

PRIOR FILING DATE: 2000-01-11

PRIOR APPLICATION NUMBER: 09/370,265

PRIOR FILING DATE: 1999-08-09

PRIOR APPLICATION NUMBER: PCT/US99/16180

PRIOR FILING DATE: 1999-07-16

PRIOR APPLICATION NUMBER: 09/350,836

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: 09/273,447

PRIOR FILING DATE: 1999-03-19

PRIOR APPLICATION NUMBER: 09/244,444

PRIOR FILING DATE: 1999-02-04

PRIOR APPLICATION NUMBER: 09/122,449

PRIOR FILING DATE: 1998-07-24

PRIOR APPLICATION NUMBER: 09/118,205

PRIOR FILING DATE: 1998-07-16

NUMBER OF SEQ ID NOS: 60

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 5

LENGTH: 428

TYPE: PRT

ORGANISM: Homo sapiens

US-09-608-285A-5

Query Match

100.0%; Score 2250; DB 4; Length 428;

Best Local Similarity

100.0%; Pred. No. 6.4e-248;

Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy

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Db

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Qy

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Qy

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Qy

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301

EPCYAEVLRVVRGKHLQHPVEVQSGFYAFSYYYDRAVDTMDIDYKGGILKVEDPERKAR

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Qy

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420

Db

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420

Qy

421

LQSLGISH 428

Db

421

LQSLGISH 428

RESULT 3

US-09-240-639-6

Sequence 5, Application US/09240639

Patent No. 6350447

GENERAL INFORMATION:

APPLICANT: Chadwick, Brian Paul

APPLICANT: Frischauf, Anna-Maria

TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE

TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS

FILE REFERENCE: 9598-066

CURRENT APPLICATION NUMBER: US/09/240,639

CURRENT FILING DATE: 1998-01-29

NUMBER OF SEQ ID NOS: 29

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 6

LENGTH: 428

TYPE: PRT

ORGANISM: Homo sapiens

US-09-240-639-6

Query Match

100.0%; Score 2250; DB 4; Length 428;

Best Local Similarity

100.0%; Pred. No. 6.4e-248;

Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

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Db

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240

QY 241 SYLGFLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEVF 300
DB 241 SYLGFLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEVF 300
QY 301 EPCYAEVLVRVGRKGLHQPVEEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
DB 301 EPCYAEVLVRVGRKGLHQPVEEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
QY 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQTLTKKVNNIETGALGATFHL 420
DB 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQTLTKKVNNIETGALGATFHL 420
QY 421 LQSLGISH 428
DB 421 LQSLGISH 428

RESULT 4

US-09-240-639-9

; Sequence 9, Application US/09240639

; Patent No. 6350447

; GENERAL INFORMATION:

; APPLICANT: Chadwick, Brian Paul

; APPLICANT: Frischau, Anna-Maria

; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE

; FILE REFERENCE: POLYPEPTIDES AND NUCLEIC ACIDS

; CURRENT APPLICATION NUMBER: US/09/240,639

; CURRENT FILING DATE: 1998-01-29

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: Patent in Ver. 2.0

; SEQ ID NO 9

; LENGTH: 428

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-240-639-9

Query Match 100.0%; Score 2250; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 6.4e-248;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MATSWGTVFVFMVLVSCVCSAVSHRNQOTWFBGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
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DB 61 RIHYVTFVQKMPGQLPILGEVFDVSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
QY 121 KKTPEVLKATAGLRLPEHKAKALLFEVKEIFRKSPLVPKGSVINDGEGTAAWVTV 180
DB 121 KKTPEVLKATAGLRLPEHKAKALLFEVKEIFRKSPLVPKGSVINDGEGTAAWVTV 180
QY 181 NFLTGQLHGHROETVGTDLGGASTQITFLPQFEKTLQTPRGYLTSPFNFNSTYKLYTH 240
DB 181 NFLTGQLHGHROETVGTDLGGASTQITFLPQFEKTLQTPRGYLTSPFNFNSTYKLYTH 240
QY 241 SYLGFLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEVF 300
DB 241 SYLGFLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEVF 300
QY 301 EPCYAEVLVRVGRKGLHQPVEEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
DB 301 EPCYAEVLVRVGRKGLHQPVEEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
QY 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQTLTKKVNNIETGALGATFHL 420
DB 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQTLTKKVNNIETGALGATFHL 420
QY 421 LQSLGISH 428
DB 421 LQSLGISH 428

RESULT 5

US-09-350-836B-3

; Sequence 3, Application US/09350836B

; Patent No. 6387645

; GENERAL INFORMATION:

; APPLICANT: Ford, John

; APPLICANT: Mulero, Julio

; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE

; FILE REFERENCE: POLYPEPTIDES

; CURRENT APPLICATION NUMBER: US/09/350,836B

; CURRENT FILING DATE: 1999-07-09

; PRIOR APPLICATION NUMBER: 09/273,447

; PRIOR FILING DATE: 1999-03-19

; PRIOR APPLICATION NUMBER: 09/118,205

; PRIOR FILING DATE: 1998-07-16

; PRIOR APPLICATION NUMBER: 09/122,449

; PRIOR FILING DATE: 1998-07-24

; PRIOR APPLICATION NUMBER: 09/244,444

; PRIOR FILING DATE: 1999-02-04

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: Patent in Ver. 2.0

; SEQ ID NO 3

; LENGTH: 428

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-350-836B-3

Query Match 100.0%; Score 2250; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 6.4e-248;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATSWGTVFVFMVLVSCVCSAVSHRNQOTWFBGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSWGTVFVFMVLVSCVCSAVSHRNQOTWFBGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
QY 61 RIHYVTFVQKMPGQLPILGEVFDVSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
DB 61 RIHYVTFVQKMPGQLPILGEVFDVSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
QY 121 KKTPEVLKATAGLRLPEHKAKALLFEVKEIFRKSPLVPKGSVINDGEGTAAWVTV 180
DB 121 KKTPEVLKATAGLRLPEHKAKALLFEVKEIFRKSPLVPKGSVINDGEGTAAWVTV 180
QY 181 NFLTGQLHGHROETVGTDLGGASTQITFLPQFEKTLQTPRGYLTSPFNFNSTYKLYTH 240
DB 181 NFLTGQLHGHROETVGTDLGGASTQITFLPQFEKTLQTPRGYLTSPFNFNSTYKLYTH 240
QY 241 SYLGFLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEVF 300
DB 241 SYLGFLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEVF 300
QY 301 EPCYAEVLVRVGRKGLHQPVEEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
DB 301 EPCYAEVLVRVGRKGLHQPVEEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
QY 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQTLTKKVNNIETGALGATFHL 420
DB 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQTLTKKVNNIETGALGATFHL 420
QY 421 LQSLGISH 428
DB 421 LQSLGISH 428

RESULT 6

US-09-350-836B-5

; Sequence 5, Application US/09350836B

; Patent No. 6387645

; GENERAL INFORMATION:

; APPLICANT: Ford, John

; APPLICANT: Mulero, Julio

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; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/35761
; CURRENT APPLICATION NUMBER: US/09/350,836B
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; TYPE: PRT
; LENGTH: 428
; ORGANISM: Homo sapiens
US-09-350-836B-5

Query Match      100.0%; Score 2250; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 6.4e-248;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATSGTVPFPMVLVVCVCSAVSHRNQQTWFEGLFLSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSGTVPFPMVLVVCVCSAVSHRNQQTWFEGLFLSSMCPINVSASTLYGIMFDAGSTGT 60

QY 61 RIHYVTFVQKMPQQLPILEGEVDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
DB 61 RIHYVTFVQKMPQQLPILEGEVDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120

QY 61 RIHYVTFVQKMPQQLPILEGEVDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
DB 61 RIHYVTFVQKMPQQLPILEGEVDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120

QY 121 KKTPTVLKATAGRLRLPEHKAKALLFEVKIIPKSPFLVPKGSVIMDSDEGLAWVTV 180
DB 121 KKTPTVLKATAGRLRLPEHKAKALLFEVKIIPKSPFLVPKGSVIMDSDEGLAWVTV 180

QY 181 NFLTQGLHGHROETVGTDLGGASTQITFLPQFEKTLQTPRGYLTSEMFNSTYKLYTH 240
DB 181 NFLTQGLHGHROETVGTDLGGASTQITFLPQFEKTLQTPRGYLTSEMFNSTYKLYTH 240

QY 241 SYLGFGKLAARLATIAGALETEGTDGHTFRSACLPRWLEAWIFGGVKYQYGGNQEYGVF 300
DB 241 SYLGFGKLAARLATIAGALETEGTDGHTFRSACLPRWLEAWIFGGVKYQYGGNQEYGVF 300

QY 301 EPCYAEVLVRVVRGKLPQEVQSGFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
DB 301 EPCYAEVLVRVVRGKLPQEVQSGFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360

QY 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQTKKNNIETGWLGAATPHL 420
DB 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQTKKNNIETGWLGAATPHL 420

QY 421 LQSLGISH 428
DB 421 LQSLGISH 428

RESULT 7
US-09-370-265-3
; Sequence 3, Application US/09370265
; Patent No. 6447771
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; FILE REFERENCE: 28111/35908
; CURRENT APPLICATION NUMBER: US/09/370,265
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; EARLIER FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: 09/350,836
; EARLIER FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: 09/273,447
; EARLIER FILING DATE: 1999-07-16
; EARLIER APPLICATION NUMBER: 09/350,836
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; EARLIER FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: 09/273,447
; EARLIER FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: 09/244,444
; EARLIER FILING DATE: 1999-02-04
; EARLIER APPLICATION NUMBER: 09/122,449
; EARLIER FILING DATE: 1998-07-24
; EARLIER APPLICATION NUMBER: 09/118,205
; EARLIER FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; TYPE: PRT
; LENGTH: 428
; ORGANISM: Homo sapiens
US-09-370-265-3

Query Match      100.0%; Score 2250; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 6.4e-248;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATSGTVPFPMVLVVCVCSAVSHRNQQTWFEGLFLSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSGTVPFPMVLVVCVCSAVSHRNQQTWFEGLFLSSMCPINVSASTLYGIMFDAGSTGT 60

QY 61 RIHYVTFVQKMPQQLPILEGEVDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
DB 61 RIHYVTFVQKMPQQLPILEGEVDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120

QY 121 KKTPTVLKATAGRLRLPEHKAKALLFEVKIIPKSPFLVPKGSVIMDSDEGLAWVTV 180
DB 121 KKTPTVLKATAGRLRLPEHKAKALLFEVKIIPKSPFLVPKGSVIMDSDEGLAWVTV 180

QY 181 NFLTQGLHGHROETVGTDLGGASTQITFLPQFEKTLQTPRGYLTSEMFNSTYKLYTH 240
DB 181 NFLTQGLHGHROETVGTDLGGASTQITFLPQFEKTLQTPRGYLTSEMFNSTYKLYTH 240

QY 241 SYLGFGKLAARLATIAGALETEGTDGHTFRSACLPRWLEAWIFGGVKYQYGGNQEYGVF 300
DB 241 SYLGFGKLAARLATIAGALETEGTDGHTFRSACLPRWLEAWIFGGVKYQYGGNQEYGVF 300

QY 301 EPCYAEVLVRVVRGKLPQEVQSGFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
DB 301 EPCYAEVLVRVVRGKLPQEVQSGFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360

QY 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQTKKNNIETGWLGAATPHL 420
DB 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQTKKNNIETGWLGAATPHL 420

QY 421 LQSLGISH 428
DB 421 LQSLGISH 428

RESULT 8
US-09-370-265-5
; Sequence 5, Application US/09370265
; Patent No. 6447771
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; FILE REFERENCE: 28111/35908
; CURRENT APPLICATION NUMBER: US/09/370,265
; PRIOR FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: PCT/US99/16180
; EARLIER FILING DATE: 1999-07-16
; EARLIER APPLICATION NUMBER: 09/350,836
; EARLIER FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: 09/273,447
; EARLIER FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: 09/244,444
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; EARLIER FILING DATE: 1999-02-04
; EARLIER APPLICATION NUMBER: 09/122,449
; EARLIER FILING DATE: 1998-07-24
; EARLIER APPLICATION NUMBER: 09/118,205
; EARLIER FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-370-265-5

Query Match 100.0%; Score 2250; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 6.4e-248; Indels 0; Gaps 0;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATSWGTVPFVPMVSVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSWGTVPFVPMVSVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60

QY 61 RIHVYTFVQKMPGOLPILLEGVDSVKPGLSAPVDQPKQGAETVOGLLEVAKDSIPRSHW 120
DB 61 RIHVYTFVQKMPGOLPILLEGVDSVKPGLSAPVDQPKQGAETVOGLLEVAKDSIPRSHW 120

QY 121 KTFPVVLKATAGLRLLPEHKAKALLPEVKEIFRKSPLVPKGSVSIINDSDGGLAWTV 180
DB 121 KTFPVVLKATAGLRLLPEHKAKALLPEVKEIFRKSPLVPKGSVSIINDSDGGLAWTV 180

QY 181 NFLTQGLHGHROETVGTDLGGASTQITFLPOPEKTLQTPRGYLTSPFENFSTYKLYTH 240
DB 181 NFLTQGLHGHROETVGTDLGGASTQITFLPOPEKTLQTPRGYLTSPFENFSTYKLYTH 240

QY 241 SYLGFGLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGVF 300
DB 241 SYLGFGLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGVF 300

QY 301 EPCYAEVLVRVVRGKLHQPVEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDPERKAR 360
DB 301 EPCYAEVLVRVVRGKLHQPVEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDPERKAR 360

QY 361 EVCNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQTKKNNIETGVALGATFHL 420
DB 361 EVCNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQTKKNNIETGVALGATFHL 420

QY 421 LQSLGISH 428
DB 421 LQSLGISH 428

RESULT 9
US-09-557-800C-3
; Sequence 3, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19

; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-557-800C-3

Query Match 100.0%; Score 2250; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 6.4e-248; Indels 0; Gaps 0;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATSWGTVPFVPMVSVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSWGTVPFVPMVSVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60

QY 61 RIHVYTFVQKMPGOLPILLEGVDSVKPGLSAPVDQPKQGAETVOGLLEVAKDSIPRSHW 120
DB 61 RIHVYTFVQKMPGOLPILLEGVDSVKPGLSAPVDQPKQGAETVOGLLEVAKDSIPRSHW 120

QY 121 KTFPVVLKATAGLRLLPEHKAKALLPEVKEIFRKSPLVPKGSVSIINDSDGGLAWTV 180
DB 121 KTFPVVLKATAGLRLLPEHKAKALLPEVKEIFRKSPLVPKGSVSIINDSDGGLAWTV 180

QY 181 NFLTQGLHGHROETVGTDLGGASTQITFLPOPEKTLQTPRGYLTSPFENFSTYKLYTH 240
DB 181 NFLTQGLHGHROETVGTDLGGASTQITFLPOPEKTLQTPRGYLTSPFENFSTYKLYTH 240

QY 241 SYLGFGLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGVF 300
DB 241 SYLGFGLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGVF 300

QY 301 EPCYAEVLVRVVRGKLHQPVEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDPERKAR 360
DB 301 EPCYAEVLVRVVRGKLHQPVEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDPERKAR 360

QY 361 EVCNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQTKKNNIETGVALGATFHL 420
DB 361 EVCNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQTKKNNIETGVALGATFHL 420

QY 421 LQSLGISH 428
DB 421 LQSLGISH 428

RESULT 10
US-09-557-800C-5
; Sequence 5, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447

; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-557-800C-5

Query Match 100.0%; Score 2250; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 6.4e-248;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATSGTVPFVFLVSCVSAVSHRNQQTWTFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSGTVPFVFLVSCVSAVSHRNQQTWTFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60

QY 61 RIHYVTFVQKMPGQLPILGEVFDVSKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
DB 61 RIHYVTFVQKMPGQLPILGEVFDVSKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120

QY 121 KKTVPVLKATAGLRLLPEHKAKALLFEVKIIFRKSPPFLVPKGSVSIINQSPDEGILAWVTV 180
DB 121 KKTVPVLKATAGLRLLPEHKAKALLFEVKIIFRKSPPFLVPKGSVSIINQSPDEGILAWVTV 180

QY 181 NFLTQQLHGRHROETVGTDLGGASTQITFLPQFEKTLQOTPRGYLTSFEMNSTYKLYTH 240
DB 181 NFLTQQLHGRHROETVGTDLGGASTQITFLPQFEKTLQOTPRGYLTSFEMNSTYKLYTH 240

QY 241 SYLGFGLKAARLATIAGALETEGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
DB 241 SYLGFGLKAARLATIAGALETEGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300

QY 301 EPCYAEVLVRVVRGKHOPEVQSGFYAFSYYYDRAVDTMDIDYKGGILKVEDPERKAR 360
DB 301 EPCYAEVLVRVVRGKHOPEVQSGFYAFSYYYDRAVDTMDIDYKGGILKVEDPERKAR 360

QY 361 EVCNMLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKVNNIETGALGATPHL 420
DB 361 EVCNMLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKVNNIETGALGATPHL 420

QY 421 LQSLGISH 428
DB 421 LQSLGISH 428

RESULT 11
US-09-370-625A-3
; Sequence 3, Application US/09370625A
; Patent No. 6600032
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
; FILE REFERENCE: 28110/35908
; CURRENT FILING DATE: 1999-08-09
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 428

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-370-625A-3

Query Match 100.0%; Score 2250; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 6.4e-248;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATSGTVPFVFLVSCVSAVSHRNQQTWTFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSGTVPFVFLVSCVSAVSHRNQQTWTFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60

QY 61 RIHYVTFVQKMPGQLPILGEVFDVSKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
DB 61 RIHYVTFVQKMPGQLPILGEVFDVSKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120

QY 121 KKTVPVLKATAGLRLLPEHKAKALLFEVKIIFRKSPPFLVPKGSVSIINQSPDEGILAWVTV 180
DB 121 KKTVPVLKATAGLRLLPEHKAKALLFEVKIIFRKSPPFLVPKGSVSIINQSPDEGILAWVTV 180

QY 181 NFLTQQLHGRHROETVGTDLGGASTQITFLPQFEKTLQOTPRGYLTSFEMNSTYKLYTH 240
DB 181 NFLTQQLHGRHROETVGTDLGGASTQITFLPQFEKTLQOTPRGYLTSFEMNSTYKLYTH 240

QY 241 SYLGFGLKAARLATIAGALETEGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
DB 241 SYLGFGLKAARLATIAGALETEGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300

QY 301 EPCYAEVLVRVVRGKHOPEVQSGFYAFSYYYDRAVDTMDIDYKGGILKVEDPERKAR 360
DB 301 EPCYAEVLVRVVRGKHOPEVQSGFYAFSYYYDRAVDTMDIDYKGGILKVEDPERKAR 360

QY 361 EVCNMLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKVNNIETGALGATPHL 420
DB 361 EVCNMLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQTKKVNNIETGALGATPHL 420

QY 421 LQSLGISH 428
DB 421 LQSLGISH 428

RESULT 12
US-09-370-625A-5
; Sequence 5, Application US/09370625A
; Patent No. 6600032
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDE
; FILE REFERENCE: 28110/35908
; CURRENT FILING DATE: 1999-08-09
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-370-625A-5

Query Match 100.0%; Score 2250; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 6.4e-248;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATSGTVPFVFLVSCVSAVSHRNQQTWTFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSGTVPFVFLVSCVSAVSHRNQQTWTFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60

QY 61 RIHVYTFVKMPGQLPILGEVFDSPKGLSAPVDPKQGAETVQGLLEVAKDSIPRSHW 120
DB 61 RIHVYTFVKMPGQLPILGEVFDSPKGLSAPVDPKQGAETVQGLLEVAKDSIPRSHW 120
QY 121 KKTTPVVLKATAGRLRLPEHAKALLFEVKEIFRKSPLVPKGSVSIIMDSDEGILAWTV 180
DB 121 KKTTPVVLKATAGRLRLPEHAKALLFEVKEIFRKSPLVPKGSVSIIMDSDEGILAWTV 180
QY 181 NFLTGOLHGHROETVGTDLGGASTQITFLPOPEKTLQOTPRGYLTSPFNFSTYKLYTH 240
DB 181 NFLTGOLHGHROETVGTDLGGASTQITFLPOPEKTLQOTPRGYLTSPFNFSTYKLYTH 240
QY 241 SYLGFLKAARLALIGALETEGDTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
DB 241 SYLGFLKAARLALIGALETEGDTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
QY 301 EPCYAEVLVRVGRKLGHPQEEVQSGSFYAFSYYVDRAVDTMDIDYKGGILKVEDFERKAR 360
DB 301 EPCYAEVLVRVGRKLGHPQEEVQSGSFYAFSYYVDRAVDTMDIDYKGGILKVEDFERKAR 360
QY 361 EVCNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQTKKNNIETGVALGATPHL 420
DB 361 EVCNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQTKKNNIETGVALGATPHL 420
QY 421 LQSLGISH 428
DB 421 LQSLGISH 428

RESULT 13
US-09-608-285A-7
; Sequence 7, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1998-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-608-285A-7

method of antibody

Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MATSGTGVFFMLVWSCVSAVSHRNQQTWFEIGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSGTGVFFMLVWSCVSAVSHRNQQTWFEIGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
QY 61 RIHVYTFVKMPGQLPILGEVFDSPKGLSAPVDPKQGAETVQGLLEVAKDSIPRSHW 120
DB 61 RIHVYTFVKMPGQLPILGEVFDSPKGLSAPVDPKQGAETVQGLLEVAKDSIPRSHW 120
QY 121 KKTTPVVLKATAGRLRLPEHAKALLFEVKEIFRKSPLVPKGSVSIIMDSDEGILAWTV 180
DB 121 KKTTPVVLKATAGRLRLPEHAKALLFEVKEIFRKSPLVPKGSVSIIMDSDEGILAWTV 180
QY 181 NFLTGOLHGHROETVGTDLGGASTQITFLPOPEKTLQOTPRGYLTSPFNFSTYKLYTH 240
DB 181 NFLTGOLHGHROETVGTDLGGASTQITFLPOPEKTLQOTPRGYLTSPFNFSTYKLYTH 240
QY 241 SYLGFLKAARLALIGALETEGDTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
DB 241 SYLGFLKAARLALIGALETEGDTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
QY 301 EPCYAEVLVRVGRKLGHPQEEVQSGSFYAFSYYVDRAVDTMDIDYKGGILKVEDFERKAR 360
DB 301 EPCYAEVLVRVGRKLGHPQEEVQSGSFYAFSYYVDRAVDTMDIDYKGGILKVEDFERKAR 360
QY 361 EVCNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQTKKNNIETGVALGATPHL 420
DB 361 EVCNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQTKKNNIETGVALGATPHL 420
QY 421 LQSLGISH 428
DB 421 LQSLGISH 428

RESULT 14
US-09-350-836B-7
; Sequence 7, Application US/09350836B
; Patent No. 6387645
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; FILE REFERENCE: 28110/35761
; CURRENT APPLICATION NUMBER: US/09/350,836B
; CURRENT FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-350-836B-7

method of ID inhibition

Query Match 99.3%; Score 2235; DB 4; Length 428;
Best Local Similarity 99.3%; Pred. No. 3.3e-246;
Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MATSGTGVFFMLVWSCVSAVSHRNQQTWFEIGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSGTGVFFMLVWSCVSAVSHRNQQTWFEIGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
QY 61 RIHVYTFVKMPGQLPILGEVFDSPKGLSAPVDPKQGAETVQGLLEVAKDSIPRSHW 120

Query Match 99.3%; Score 2235; DB 4; Length 428;
Best Local Similarity 99.3%; Pred. No. 3.3e-246;

Db 61 RIHVYFVQKMPQLPILGEGVDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
Qy 121 KKTPTVVKATAGLRLPEHKAKALLFEVKEIFRKSPLVPKGSVIMTQDEGIFAWVTY 180
Db 121 KKTPTVVKATAGLRLPEHKAKALLFEVKEIFRKSPLVPKGSVIMTQDEGIFAWVTY 180
Qy 181 NPLTQOLHGHQRTVGTDLGGASTQITFLPQFEKTLBQTPRGYLTSPENFNSTYKLYTH 240
Db 181 NPLTQOLHGHQRTVGTDLGGASTQITFLPQFEKTLBQTPRGYLTSPENFNSTYKLYTH 240
Qy 241 SYLGFGKAAARLATTGALTEGTGHTFRSACLPRWLEAEWIFGGVKKYQYGGNQEVEVGF 300
Db 241 SYLGFGKAAARLATTGALTEGTGHTFRSACLPRWLEAEWIFGGVKKYQYGGNQEVEVGF 300
Qy 301 EPCYAEVLVRVVRGKLHQPVEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
Db 301 EPCYAEVLVRVVRGKLHQPVEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
Qy 361 EPCYAEVLVRVVRGKLHQPVEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
Db 361 EPCYAEVLVRVVRGKLHQPVEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
Qy 421 LQSLGISH 428
Db 421 LQSLGISH 428

method of doing

RESULT 15
US-09-370-265-7
Sequence, Application US/09370265
Patent No. 6447771
GENERAL INFORMATION
APPLICANT: Eads, John
APPLICANT: Mulero, Julio
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
FILE REFERENCE: 28111/35908
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: PCT/US99/16180
EARLIER FILING DATE: 1999-07-16
EARLIER APPLICATION NUMBER: 09/350,836
EARLIER FILING DATE: 1999-07-09
EARLIER APPLICATION NUMBER: 09/273,447
EARLIER FILING DATE: 1999-03-19
EARLIER APPLICATION NUMBER: 09/244,444
EARLIER FILING DATE: 1999-02-04
EARLIER APPLICATION NUMBER: 09/122,449
EARLIER FILING DATE: 1998-07-24
EARLIER APPLICATION NUMBER: 09/118,205
EARLIER FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 428
TYPE: PRI
ORGANISM: Homo sapiens
US-09-370-265-7

Query Match 99.3%; Score 2235; DB 4; Length 428;
Best Local Similarity 99.3%; Pred. No. 3.3e-246;
Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MATSNGTVFPMVVCVCSAVSHRNQOTWFGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
Db 1 MATSNGTVFPMVVCVCSAVSHRNQOTWFGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
Qy 61 RIHVYFVQKMPQLPILGEGVDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
Db 61 RIHVYFVQKMPQLPILGEGVDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
Qy 121 KKTPTVVKATAGLRLPEHKAKALLFEVKEIFRKSPLVPKGSVIMTQDEGIFAWVTY 180

Db 121 KKTPTVVKATAGLRLPEHKAKALLFEVKEIFRKSPLVPKGSVIMTQDEGIFAWVTY 180
Qy 181 NPLTQOLHGHQRTVGTDLGGASTQITFLPQFEKTLBQTPRGYLTSPENFNSTYKLYTH 240
Db 181 NPLTQOLHGHQRTVGTDLGGASTQITFLPQFEKTLBQTPRGYLTSPENFNSTYKLYTH 240
Qy 241 SYLGFGKAAARLATTGALTEGTGHTFRSACLPRWLEAEWIFGGVKKYQYGGNQEVEVGF 300
Db 241 SYLGFGKAAARLATTGALTEGTGHTFRSACLPRWLEAEWIFGGVKKYQYGGNQEVEVGF 300
Qy 301 EPCYAEVLVRVVRGKLHQPVEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
Db 301 EPCYAEVLVRVVRGKLHQPVEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
Qy 361 EPCYAEVLVRVVRGKLHQPVEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 420
Db 361 EPCYAEVLVRVVRGKLHQPVEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 420
Qy 421 LQSLGISH 428
Db 421 LQSLGISH 428

Search completed: July 1, 2004, 13:50:10
Job time : 17.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 1, 2004, 13:43:42 ; Search time 16.5 Seconds

(without alignments)
2495.150 Million cell updates/sec

Title: US-10-091-085-3

Perfect score: 2250

Sequence: 1 MATSWGTVFFMLVVCVCSA.....ETGWALGATFHLLQSLGISH 428

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.78.*

2: PIR1.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	616.5	27.4	479	2	T23508	hypothetical prote
2	536.5	23.9	556	2	T39109	probable guanosine
3	489	21.7	455	2	S48859	nucleoside triphos
4	483.5	21.5	518	2	A40732	guanosine-diphosph
5	446.5	19.8	454	2	JC4616	aprase (EC 3.6.1.
6	425.5	18.9	516	2	G84442	probable nucleosid
7	397	17.6	483	2	D86276	hypothetical prote
8	387.5	17.2	485	2	T34147	hypothetical prote
9	372.5	16.6	557	2	T16696	hypothetical prote
10	372	16.5	630	2	S50463	hypothetical prote
11	351	15.6	510	2	I56242	lymphoid cell acti
12	347	15.4	572	2	T40856	probable nucleotid
13	329.5	14.6	405	2	E86276	hypothetical prote
14	274	12.2	1052	2	T04439	hypothetical prote
15	248	11.0	508	2	C86276	7A19.33 protein -
16	139	6.1	628	2	A55421	nucleoside-triphos
17	110	4.9	497	1	JC2192	subtilisin-like pr
18	106.5	4.7	553	1	GBPSV	gene 1 protein - s
19	105.5	4.7	774	2	T14555	DNA polymerase hom
20	104.5	4.6	684	2	T47694	probable serine/th
21	104.5	4.6	4427	2	PN0637	polyketide synthas
22	102.5	4.6	1019	2	T40813	probable cell divi
23	101.5	4.5	535	2	P97910	glucan 1,6-alpha-g
24	101.5	4.5	1151	2	H71347	hypothetical prote
25	99.5	4.4	535	2	C95040	glucan 1,6-alpha-g
26	99.5	4.4	548	1	HYBSS	bacillolysin (EC 3
27	97.5	4.3	604	2	F89453	protein F35H12.4 [
28	97.5	4.3	654	2	AG3522	iron-regulated out
29	97	4.3	1220	2	T18291	patched protein -

hypothetical prote
fatty-acyl-CoA syn
subtilisin-like pr
hypothetical prote
probable phosphos
subtilisin-like pr
subtilisin-like pr
subtilisin-like pr
coproporphyrinogen
H⁺-transporting tw
glycine hydroxymet
t-plasminogen acti
glucanase kinase g
probable ferric si
phosphatidylserine
succinyl-diaminopi

ALIGNMENTS

RESULT 1

T23508

hypothetical protein K08H10.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000

C:Accession: T23508

R:Gardner, A.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19750

A:Accession: T23508

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-479 <WIL>

A:Cross-references: EMBL:Z83113; PIDN:CAB05544.1; GSPDB:GN00023; CSDP:K08H10.4

A:Experimental source: clone K08H10

C:Genetics:

A:Gene: CSDP:K08H10.4

A:Map position: 5

A:Introns: 36/3; 83/3; 189/1; 300/2; 412/3

C:Superfamily: nucleoside triphosphatase chromatin-associated

Query Match 27.4%; Score 616.5; DB 2; Length 479;
Best Local Similarity 34.3%; Pred. No. 1.3e-43;
Matches 150; Conservative 81; Mismatches 167; Indels 39; Gaps 16;

QY	9	FMLVVS---CVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGTRHVT	66
DB	6	FSILLISFSLSSVVTTKQY-WCHGDGVLN---NQHTCRFTTIVIDAGSTGTRLLYK	60
QY	67	FVQK-----MPQLPILEGEVDSVKGLSAFVPOPKQCAETVQGLLEVAKDSIPRSH	119
DB	61	FIDHPAIAHSGMPFK---VEKEIFQEVKPOLSSFAKSPSSAADSLEPLLQARKEVPHEM	117
QY	120	WKTPVVLKATAGRLRLPEHKAKALFEVKE-IFRKSPLVLKGVSVIMGDSBGLIAWV	178
DB	118	WEXTPTLTKATAGRLRLPGDMADDDILESVEERIFNSGFFAAPPDVAVNMFSGDEGVSWF	177
QY	179	TNVLATQLH-----GHR---QETVGLDGGASTQITPLPOFEXTLEOTPRGLTSFE	229
DB	178	TLNILETFTDPTVGHKFAHRSVAAPDLGGSTQLTWPNNEAVFSHV-GYERDID	236
QY	230	MFNSTYKLYTHSYGLFGLKAARLATIQALETG--TDGHTFRACLPFWLE-AEWIPGVV	286
DB	237	PFCHIRLPHTSPFLNGLIAARLNIL-QLETDNEIESTHQLITSCMPEGYQLTEWEY-AL	294
QY	287	KYQYGGNQEVCVGFECYAEVLVWR-GKLHQEEVQVGSFYAFSYVYDRAVDTMDIYE	345
DB	295	KF-WNINGSSSHSFECYGTGTTKNFVESSEIMHURELKGSPVLFSTFFDRLALMSGLVGN	353
QY	346	KGGLKVEDEFERKAREVC-----DNLENFTSGSFLCMLDSYITALLKQGFADSTVLQL	401
DB	354	EGGKIELRQFKEAAEIAACREKTEIDDGSHWMPQCLDLTYIVSLLRDGYQFEDNQPLVL	413

QY 402 TKXVNIETGVALGATE 418
Db 414 AKKIKMEVSWCQGLAF 430

RESULT 2
T39109
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T39109
R:Barrell, B.G.; Rajandream, M.A.; Quail, M.; Seegar, K.; Harris, D.
submitted to the EMBL Data Library, October 1999
A:Reference number: Z21828
A:Accession: T39109
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-556 <BAR>
A:Cross-references: EMBL:AL121741; PIDN:CA857338.1; GSPDB:GN00066; SPDB:SPAC824.08
A:Experimental source: strain 972h-; cosmid c824
C:Genetics:
A:Gene: SPDB:SPAC824.08
A:Map position: 1

Query Match 23.9%; Score 538.5; DB 2; Length 556;
Best Local Similarity 34.4%; Pred. No. 5.5e-37;
Matches 144; Conservative 61; Mismatches 157; Indels 57; Gaps 13;

QY 49 YGIMFDAGSTGTRIHYVTFVQMPQQLPILEGEVDSVKPGLSAFVDPQKQGAETVQGLL 108
Db 134 YVLMIDASTGSRVHYQFNCPNPS--PKLEEFPNTEPGLSSFAGPFGANASLDPLL 191

QY 109 EVAKDSIPRSHWKTPVVLKATAGLRLPEHKAALLFEVKEIFPKS--PFLVPKGSVSIM 167
Db 192 DYAMENVPEEYRRCSPVIAKATAGLRLTGESEKAILKSVRQHLNDEYPPFLVKGVSIL 251

QY 168 DGSDEGLAWTVNFLTQGLHGH--RQETVGLDLCGASTQITFLPQFEKTELEQTPRG--- 223
Db 252 ESMGEGIVAMITINLLGTGKATHSTVAVMDLGGASTQLVFEPRFASDGESLVGDHKK 311

QY 224 YLTSEFMENSTYKLYTHSYLGFGLKAARL-----ATLGALETEGTDGHTFRSAC 272
Db 312 VYLDYN--GEQVELYQSHSHGYGLKEARKLIHKEVLNNAEALKESLELLG-DSTSIIHPC 368

QY 273 L-----PRWEAEWIFGCVKYQGGNQGEVGPCEYAEVLVVR-----GKLHQP 318
Db 369 LHLNASLTHPDSKSEASEVVFVGPSLAHLSLQCGIAEKALYKXKCFVRPCSFNGVHQP 428

QY 319 ---BEVQSGSFYAFSYVYDRAVDTDMDIYKGGILKVEDFERKAREVC----- 363
Db 429 KTEFTPTDPSPIVLI SYFYDR-----MISLGMPTFTIEDMKYLANSVCSGGTYWQDAFSL 483

QY 364 -DNLENFTSGSPFLCMLSYTALLKDGFGFADSTVLQTKKNNIETGVALGATPHLL 421
Db 484 TDALKELKE-EPEWCLDNLNYSLSVGVIEPNRQLHTAKKIDNKELGWCIGASLSML 541

RESULT 3
S48859
nucleoside triphosphatase precursor, chromatin-associated - garden pea
C:Species: Pisum sativum (garden pea)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 29-Sep-1999
C:Accession: S65147; S48859
R:Hsieh, H.L.; Tong, C.G.; Thomas, C.; Roux, S.J.
Plant Mol. Biol. 30, 135-147, 1996
A:Title: Light-modulated abundance of an mRNA encoding a calmodulin-regulated, chromatin-associated triphosphatase
A:Reference number: S65147
A:Accession: S65147
A:Molecule type: mRNA
A:Residues: 1-455 <HS2>
A:Cross-references: EMBL:Z32743; NID:G563611; PIDN:CAA83655.1; PID:G563612
C:Superfamily: nucleoside triphosphatase chromatin-associated

C;Keywords: nucleus

Query Match 21.7%; Score 489; DB 2; Length 455;
Best Local Similarity 33.7%; Pred. No. 5.8e-33;
Matches 140; Conservative 62; Mismatches 160; Indels 54; Gaps 14;

QY 49 YGIMFDAGSTGTRIHYVTFVQMPQQLPILEGEVDSVKPGLSAFVDPQKQGAETVQGL 107
Db 44 YAVVEDAGSTGSRHVVHFQNL-DLLHIGKGVYVYKNTITPGLSSVANNPEQAASLIPL 102

QY 108 LEVAKDSIPRSHWKTPVVLKATAGLRLPEHKAALLFEVKEIF-RKSPFLVPKGSVSI 166
Db 103 LEQAEVVPDDLOQKTPFVRLGATAGLRLNGDASEKILQSDRMDLSNRSTFNQPDVSI 162

QY 167 MDGSDGILAWTVNFLTQGLHGH--RQETVGLDLCGASTQITFLPQFEKTELEQTPR--- 222
Db 163 IDGTQSGSYLWTVNVALGNLKKYKTVGVGLDGGSVQMAVAVS-KKTAKNAPKAVDG 221

QY 223 --GYLTSEFMENSTYKLYTHSYLGFGLKAARLALTLGALETEGTDGHTFRS--ACLPRWLE 278
Db 222 DDPYIKKVLKGIPIYDLVHSHYLFHFGREASRAILKL-----TPRSPNCPCLLAGPN 272

QY 279 AEWIEGCVKYQGGNQGEVGPCEYAEVLVVRGKLHQPEEVQSGSF----- 326
Db 273 GIYITSGEFPKATAYTSG--ANFNKCKNTIRKAL--KLNYPECYQNCFTGGIHWGGGNGQ 329

QY 327 ---YAFSYVYDRAVDTDMDIYKGG-ILKYDEPFERKAREVCD-NLENFTSGSPFL----- 376
Db 330 KNLFPASSSPFLPDETGWDASTPNTFLRPVDIETRAKEACALNFEDAKSTYFPFLDKKNV 389

QY 377 ---CMLDSVITALLKDGFGFADSTVLQTKKNN-----LETGWALGATPHLLQSL 424
Db 390 ASYVCMDLIYQYVLLVDGFLDPLQKITSGKBIYQDAIVEAAWPLGNVAEISAL 445

RESULT 4
A40732
guanosine-diphosphatase (EC 3.6.1.42) - yeast (Saccharomyces cerevisiae)
A:Alternate names: protein YEL042w
C:Species: Saccharomyces cerevisiae
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 02-Sep-2000
C:Accession: A40732; B40732; S30837; S50502
R:Beifon, C.; Yanagisawa, K.; Mandon, E.C.; Hausler, A.; Moremen, K.; Hirschberg, C.
J. Cell Biol. 122, 307-323, 1993
A:Title: Guanosine diphosphatase is required for protein and sphingolipid glycosylat
A:Reference number: A40732; MUID:93308137; PMID:8391537
A:Accession: A40732
A:Molecule type: DNA
A:Residues: 1-518 <ABE>
A:Cross-references: EMBL:L19560; NID:G349392; PIDN:AAA34656.1; PID:G349393
A:Note: sequence extracted from NCBI backbone (NCBIN:134708, NCBIP:134711)
A:Accession: B40732
A:Molecule type: protein
A:Residues: 125-144; 238-257; 276-281; 366-374; 399-412 <AB2>
R:Mulligan, J.T.; Dietrich, F.S.; Hennessy, K.M.; Sehl, P.; Komp, C.; Wei, Y.; Tayl
submitted to the EMBL Data Library, February 1993
A:Reference number: S30812
A:Accession: S30837
A:Molecule type: DNA
A:Residues: 1-518 <MUL>
A:Cross-references: GB:U18779; EMBL:U10830; NID:G603625; PIDN:AA865000.1; PID:G60363
R:Dietrich, F.S.
A:Description: The sequence of S. cerevisiae cosmid 8199, 8334, and 9871.
A:Reference number: S50491
A:Accession: S50502
A:Molecule type: DNA
A:Residues: 1-518 <DIE>
A:Cross-references: EMBL:U18779; NID:G603625; PIDN:AA865000.1; PID:G603637; MIPS:YEL
C:Genetics:
A:Gene: SGD:GDAL
A:Cross-references: SGD:S0000768; MIPS:YEL042w
A:Map position: 5L

RESULT 5
JC4616
apyrase (EC 3.6.1.5) precursor - potato
N;Alternate names: adenylypyrophosphatase; ATP-diphosphohydrolase
C;Species: Solanum tuberosum [potato]
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 28-May-1999
C;Accession: JC4616; PC4147
R;Handa, M.; Guidotti, G.
Biochem. Biophys. Res. Commun. 218, 916-923, 1996
A;Title: Purification and cloning of a soluble ATP-diphosphohydrolase (Apyrase) from potato
A;Reference number: JC4616; MUID:96158985; PMID:8579614
A;Accession: JC4616
A;Molecule type: mRNA
A;Residues: 1-454 <HAN>
A;Cross-references: GB:U58597; NID:gr1381632; PIDN:AAB0720.1; PID:gl381633
A;Accession: PC4147
A;Molecule type: protein
A;Residues: 53-95;96-131;132-160;236-253;332-345 <HA2>
A;Experimental source: tubers
A;Note: The authors translated the codon GCA for residue 215 as Gly
C;Comment: This enzyme belongs to a family of B-type Apyrases, and it catalyzes the hydrolysis of ATP to ADP and inorganic pyrophosphate (PPi). It has a high substrate specificity, divalent cation requirement, and is insensitive to inhibition by vanadate.
C;Genetics:
A;Gene: rrop1
C;Superfamily: nucleoside triphosphatase chromatin-associated
C;Keywords: glycoprotein; hydrolase; transmembrane protein
F;1-30/Domain: signal sequence #status predicted <SIG>
F;8-25/Domain: transmembrane #status predicted <TM>

[illegible]


```
Db 61 NURSLRYSVVDDGSGTTRIHFVGY--RISSGKPVFRGNANYASLKLHGLSNAPDDP 118
Qy 98 KQAEVTVQGLLEVAKDSIPRSHWKTTPVVLKATAGRLILPEHAKALLFEVKEIFRKSPP 157
Db 119 DGASVSLTELVEFAKGRVSKGMWIEVEVELMATAGXRLLELPVQEKILGVARRVLKSGF 178
Qy 156 LVPKGSVSMDSGSGILAWTVNLTGOLHGHROETVGTLDLGGASTQITFL-----P 211
Db 179 LFRDEWASVISGSDGVAVWVANFALGSLGDPKTTGIVELGASAGVTFVPSSEPP 238
Qy 212 QPEKTEQTPRGYLSFEMFNSTYKLYTHSYLGFGLKAARLATLAL-----ETEGTD 264
Db 239 EFSRTI-----SFG--NVTNLYSHSPLHFGNAADKLGSLSDRHNSAVEPTR 287
Qy 265 GHTPRSACLP-----WLEAWIFGGVYQYGNQGEVGFPEPCYAVLAVV 311
Db 288 EXIFDPCAPKGYNDANTQKLSGLLAESLSDSFOAGN-----YSQCRSAALTIL 341
Qy 312 RGLKHQPEEVQVQSGSFVAFYYDDRAVDITMI-----DYEGKGLLKVEDFERKAREV 362
Db 342 QDQNGRILLIAGSPLFGLGKAWLSNWSIAGERFCGEDASK--LRVKDPSLHEEDL 398
Qy 363 CONLENFTSGSPFLCMLDLSYITALLKDGFGP-ADSTVLQLTKKVNNIETGMALGA 416
Db 399 LR-----YCFSSAYIVSLHDTLGLDDEIRIGYANQAGDIPLDWALGA 442

RESULT 7
D86276
hypothetical protein F7A19.34 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 19-Nov-2002
C:Accession: D86276
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
ansen, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, K.;
ature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MID:21016719; PMID:11130712
A:Accession: D86276
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-483 <STO>
A:Cross-references: GB:AE005172; NID:G5080801; PIDN:NAD39311.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1
C:Superfamily: nucleoside triphosphatase chromatin-associated

Query Match 17.6%; Score 397; DB 2; Length 483;
Best Local Similarity 27.6%; Pred. No. 3.3e-25;
Matches 120; Conservative 71; Mismatches 162; Indels 82; Gaps 17;

Qy 32 GIFLSSMCPINVASLTLYGIMFDAGSTGTRIHY--YTFVQRMFGQLPILEGEVDP----- 84
Db 59 GSLLSRCKLR-----YSLIDAGSSGTRVHVFYGFWSGKP-----VPDFGEKH 103
Qy 85 ----SVKPGLSAFVDQPKQAEVTVQGLLEVAKDSIPRSHWKTTPVVLKATAGRLILPEHK 140
Db 104 YANILKLTGSLSSVADNPEGASVSVTKLVEPAQRIPKRMFRSDITLMATAGNRLLEVPV 163
Qy 141 AKALAFEVKEIFRKSFPVLPKGSVSMDSGSGILAWTVNLTGOLHGHROETVGTLDL 200
Db 164 QEQLLEWTRVRLRSSGFMFRDEWANYISGSDGYSWITANYALASLGLDPLETTGIVEL 223
Qy 201 GGASTQITLQPEKTLQTPRGYLSFEMFNSTYKLYTHSYLGFGLKAARLATLGALET 260
Db 224 GGASQVTV-----SSEHVPPEYSRTIAYGNISYTIYSHSFLDYKDAALKLEKLN 278
```

RESULT 8

T34147

hypothetical protein C33H5.14 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 17-Mar-2000

C:Accession: T34147

R:Bradshaw, H.; Stellyes, L.

submitted to the EMBL Data Library, November 1995

A:Description: The sequence of C. elegans cosmid C33H5.

A:Reference number: Z21482

A:Accession: T34147

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-485

A:Cross-references: EMBL:U41007; PIDN:AAA82272.1; CESP:C33H5.14

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP:C33H5.14

A:Introns: 22/1; 83/1; 120/2; 167/1; 269/3; 399/3

C:Superfamily: nucleoside triphosphatase chromatin-associated

Query Match 17.2%; Score 387.5; DB 2; Length 485;

Best Local Similarity 27.7%; Pred. No. 2.1e-24;

Matches 120; Conservative 84; Mismatches 152; Indels 77; Gaps 18;

Qy 49 YGIMFDAGSTGTRIHYVTVQKMPQLPILEGEVDS-----VKPGLSAFVDQPKQAE 102

Db 25 YGVICDAGSSGTRULFVIT-LKPLSGGLTNIDTLHESEPVVKVKTPLGLSFGDKPEQVVE 83

Qy 103 TVQGLLEVAKDSIPRSHWKTTPVVLKATAGRLILPEHAKALLFEVKEIFRKSPP-LVPK 161

Db 84 YLTPLRPAEHHIPEYQIGETDLIFATAGWELLPEAQKDAIKNLQNLKSVTALRVSD 143

Qy 162 GSVSIMDSGSGILAWTVNLTGOLHGHROETVGTLDLGGASTQITFLQPEK----- 215

Db 144 SNIRIIDGMEGIYSWIAVAVILGRFDKENDSKVGMIDMGASVQIAPEIANEKESYNGG 203

Qy 216 TLEQTPRGYLSFEMFNSTYKLYTHSYLGFGLKAARLATLGALETGDTGHTFPRACLP 275

Db 204 NYVEINLGSITNEDYK--YKIYSTFLGYGANGLKXENSLVKSGNS-----NDSCSPR 257

Qy 276 WLEAWIFGGVYQYGNQGEVGFPEPCYAVLVRVTKLHOPE----- 319

Db 258 GLNR--LIG-----EFTVNGTGE--WDVCLAQVSLI-GDKAQSPCNPTCFLRNVIAPSV 308

Qy 320 EVQSGSFVAFS--YYDRAVDITMDIYEKGGILKVEDFERKAREVC-----DNLENFTSGP 374

Db 309 NLSTVQLXGSEYVYVTS-----NFGSGGEYHVKQFTDEVRYKQCKDWDNDIQDFKENE 362

Qy 375 F-----LCMDLSYITALLKDGFGFADST--VLQTKQNNIETGMALGA----- 416

Db 363 FPNADIERLGTNCFKAAWTVSVLHDGFN-VDKTKHLPQSVLKIAGEEMQWALGAMLYHSK 421

Qy 417 --TFHLLQSLGIS 427

Db 422 DLKFNLEQUEVA 434

Db		152	VERSLSNYPF--DFQGARILTGOBEGAYGHITINYLKGXPSQXRWFISVIVPTWNNQETP	209
Qy		196	GTLDLGGASTOITFLPOFEKTLBOTPRGYITSPEMFNSYKYLYTHSYLGFLGAARLATL	255
Db		210	GALDLGGASTOWTVPO- NOTIE- SPDNAL-QFRLYGKDYNVYTHSYFLCYGDQDQALWOGL	266
Qy		256	GALTEGTDGHTFSACL-----PWLEAEWIFGGVKYGVCGNQGE	297
Db		267	-AKDIQVASNEILDPCFHPCYKKVNVSPLYKTCTKGFEMTLPPQSPSIOIGIGN----	321
Qy		298	VGFPCVAEVLUV-----VEGKLHQPEEVQORGSFYAFSYYYDRAVDVTOMIDYE	345
Db		322	--YQCCHOSILELFNTSYCPYSQCAFNGLFPPLQSGDFGAFSAF-YFVMKFNL---LTSE	375
Qy		346	KGGILKVBDPERK-AREVCNDLENFTSG--SPFL----CMDLSYITALLXDGFGP-ADS-T	397
Db		376	KVSQEKTVMKKKCAQPWEIEKITSYAGVKEVILSEYCFSGTYILSLLLQGHHFTADSWE	435
Qy		398	VLQLTKKNVNIETGWALGATPHL	420
Db		436	HIFHGKIQQSDAGWTGLGYMLN	458

RESULT 12

T40855
probable nucleotide phosphatase - fission yeast (*Schizosaccharomyces pombe*)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T40855
R:Kampspeger, U.; Pohl, T.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1999
A:Reference number: Z21952
A:Accession: T40855
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-572 <RAM>
A:Cross-references: EMBL:AL121783; PIDN:CA857847.1; GSPDB:GN00068; SPDB:SPCC11E10.05C
A:Experimental source: strain 972h-; cosmid c11E10
C:Genetics:
A:Gene: SPDB:SPCC11E10.05C
A:Map position: 3

Query Match	15.4%;	Score	347;	DB	2;	Length	572;
Best Local Similarity	25.5%;	Pred. No.	6.5e-21;				
Matches	115;	Conservative	67;	Mismatches	157;	Indels	112;
Gaps	167;						
QY	49	YGMFDAGSTGTRIHHVYTP-----VQXMPGOLPILGEVFD-----SVKPGLSAFVD	95				
DB	5	YGIPIDAGSGSRLLYISWDYDTSLSDRVKKLPIETIGDGGKWSLVQFGISSPAN	64				
QY	96	QPKQ-GAETVQGLLEVAKOSIPRSHWKKTPVVLKATAGLRL--PEHKAKALLFEVKEIFR	153				
DB	65	NPKHVGGKGLKELDLFAAHPKOVHKETPVFLSATAGNELLGVDANKILSHACRYIKK	124				
QY	154	KSPFLYP--KGSVSIWDGSDGILAVVYVNFPLAQGLHGRQETVGTLDLAGASTQITELP	211				
DB	125	NYDFDIPNCNSIRVDIGKABGMGLATYLLKTTSEKOTSTVGPLMDGASVQIAF--	182				
QY	212	QPEKTELEQTPRGVLTSPFEMENST-----YKLYTHSYLGFGLKAARLATLGL--	258				
DB	183	-----ELPPSQLKXVYKOSISTVHIGLQNGQQLEYFLFTVTLWLGANEAYRYLGLLI	235				
QY	259	ETP-ETDCHTFRSACUPLMLAEWIFGGVKYQVG-----NOGEVGFPEPCY	304				
DB	236	ESENGKVENTLSDPCSLR--GRTYDIDGIEFAGTGDLKQCLKLTNYLNLRKDKPCSDMPCN	293				
QY	305	AEVLRYVRGKLHOPEEVQGRSFAFSYYVDRAVTDMDIDYKGGILKVEDFEKAREVC-	363				
DB	294	FDGISI-----PPVDFANTEFVGVSFNTYNDV----FDMGSHYFPNFKYKVDYCG	343				
QY	364	-----DNLENFTSGSPFLCMLDSVITALLKDGFGFADSTV-----	398				
DB	344	TEWETVLRYLNKELTPSDTENKLEK-----LCFKASWALNYLHGEFQVPKSNSTSSND	396				

A;Accession: T04439
A;Molecule type: DNA
A;Residues: 1-1052 <BEV>
A;Cross-references: EMBL:AL021687
A;Experimental source: cultivar Columbia; BAC clone T18B16
C;Genetics:
A;Map position: 4
A;Intons: 79/3; 118/3; 217/1; 295/3; 396/3; 531/2; 815/3
A;Note: T18B16.150

Query Match 12.2%; Score 274; DB 2; Length 1052;
Best Local Similarity 24.8%; Pred. No. 2.1e-14;
Matches 107; Conservative 70; Mismatches 171; Indels 82; Gaps 19;
QY 51 IMFDASTGTGRIHVY--TFVQKMPGQLPIL-----EGEVFD--SVKPGLSAFV 94
DB 525 LVIVSITGTRAVYQASINVKDSSLPIVMKSLTEGISRKSRRAYDRMETEPGDKLV 584
QY 95 DQPKQAGET-VQGLLEVAKDSIPRSHWKTTPVVKATAGLRLPEHKAKALLPEVKEIFR 153
DB 585 NN-RTGLKTAIKPLQIAWAKQIPKNAHRTTSLFVYATAGVRLRPADSSWILGNVMSILA 643
QY 154 KSPFLVPKGSVSMDSDEGILAWVTNFLTGLHG-HROETVGTLDLGGASTQITFLPQ 212
DB 644 KSPTCRRWVKIISGTEEAYFGWTALNYQTSMLGALPKKATFGALDLGGSSLVQTFENE 703
QY 213 FEKTLQTPRGYTSFEMFNSTYKLYTHSVLGLKAA-----RLATL----- 255
DB 704 -ERTNETN---LNLRIGSVNHLSAYSLAGYGLNDADFDRSVVHLKXLPNVNMSDLIE 758
QY 256 GALETEGTGHTFSAACLPWLEAEWTFGGVKYQYGNQCEVGF-----PCYAEVLR 309
DB 759 GKLE-----MKHPLNSGNGOYICSCASSVQGGKKGSGVSIKLVGAPNKECSA 810
QY 310 VVR-GKXHOPEEVR--GSFYAFSYDDRAVDTMDIDYKGGI---LKVEDFERKAREVC 363
DB 811 LAXNAPCALPDGPRPHGQYAVSGFF-----VYRPFNLSEASLDDVLEKGRFC 862
QY 364 DN-----LENFTSGSPRL---CMLDSYITALLKDGFGPADSTV-----LQLTKKVNNIET 410
DB 863 DKAWQARTSVSPQPIEQYCFRAPHYIVSLRGLYITDKQIIIGSSITWTLGVALLS 922
QY 411 GWALGATFHL 420
DB 923 GKALSSTLGL 932

RESULT 15

C86276
7A19.33 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 18-Nov-2002
C;Accession: C86276
R;neologs, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: C86276
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-508 <STO>
A;Cross-references: GB:AE005172; NID:g5080800; PIDN:AAD39310.1; GSPDB:GN000141
C;Genetics:
A;Map position: 1
C;Superfamily: nucleoside triphosphatase chromatin-associated

Query Match 11.0%; Score 248; DB 2; Length 508;
Best Local Similarity 23.3%; Pred. No. 1.1e-12;
Matches 110; Conservative 77; Mismatches 159; Indels 126; Gaps 21;
QY 12 LVVSCVCSAV-----SERNQOTWFEIGIFLSSMCPINVSASTLYGIMFIDAGSTCT 60
DB 35 VIVACVTIALGLLFTGYILRSGRRR-----VSLHYSVIIDGSSGT 77
QY 61 RIHYTFVQKMPGQLPIL--GEVFD--PGLSAFVDQPKQAGETVQGLLEVAKDSIP 116
DB 78 RVHVEGY--RIESGKPVDFGENTYASLKLSPGLSAYADNPEGVSESVTELVEFAKRVH 135
QY 117 RSHWKTTPVVKATAGLRLPEHKAKALLPEVKEIFRKSPPVLPVPGSVSIMDGSDB--GI 174
DB 136 KGLKXSDIRLAKATAGMLLELPVQGLDVTTRVLRSGF-----DFRDEWASV 185
QY 175 LAWVTNFLTGLHGHROETVGTLDLG-----GASTQITFLPQFERTLEQTPRGYLTSP 228
DB 186 ISEILENF-----QDLMKVYMLGLLLIMRSVRLEVTFF-----STELVPSFRTL 231
QY 229 EMFNSTYKLYTHSVLGLKAAKLATLAL-----ETEGTGHTRFSAACLPWLEAEWI--- 282
DB 232 AYGNVSYNLYSHSFLDPQDAQAQEKLSLSLYNSAANSTGEGIVDPDPCIPKGVILETNLOK 291
QY 283 ----FGVKYQYGNQCEVGFPCYAEVLRVVR-----GKLHOFEEVQGS 325
DB 292 DLPGLADKGTATLQAGNFSCKSAFAFAMLQBEKGKCTYKRCSIGSIPTFN--LQGS 349
QY 326 FYAFSY--DRVDTMDI-----DYKGGILKVEDFERKAREVCNDLE 367
DB 350 FLATENFHTSKFFGLGKEMLSMILAGKRCFGSEWSK---LKVYPTFD-----ENLL 402
QY 368 NTSGPSPLCMLDSYITALLKDGFGFA-DSTVLQTKV--NNIETGWALGA 416
DB 403 RY-----CFSSAYIISMLHSLGVALDDERIKYASKAGEEDIPLDWALGA 447

Search completed: July 1, 2004, 13:49:25
Job time : 18.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 1, 2004, 13:48:47 ; Search time 44.5 Seconds
(without alignments)
2993.921 Million cell updates/sec

Title: US-10-091-085-7

Perfect score: 2252

Sequence: 1 MATSWGTFFFLVSVCSA.....ETGWLATGATFLQLSLGISH 428

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283616 residues

Total number of hits satisfying chosen parameters: 1276540

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/prodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/prodata/1/pubpaa/US09A_PUBCOMB.pep.*
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- 11: /cgn2_6/prodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep.*
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- 15: /cgn2_6/prodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2252	100.0	428	13	US-10-091-085-7
2	2252	100.0	428	13	US-10-092-063-7
3	2252	100.0	428	14	US-10-286-926-7
4	2235	99.2	428	13	US-10-091-085-3
5	2235	99.2	428	13	US-10-091-085-5
6	2235	99.2	428	13	US-10-092-063-3
7	2235	99.2	428	13	US-10-092-063-5
8	2235	99.2	428	14	US-10-286-926-3
9	2235	99.2	428	14	US-10-286-926-5
10	2235	99.2	428	15	US-10-231-913-127
11	2221	98.6	428	16	US-10-408-765A-2296
12	2089	92.8	405	13	US-10-092-063-25
13	2089	92.8	405	14	US-10-286-926-25
14	1979.5	87.9	427	15	US-10-231-913-126
15	1822.5	80.9	465	13	US-10-092-063-39

Sequence 876, App
Sequence 876, App
Sequence 27, Appl
Sequence 27, Appl
Sequence 123, Appl
Sequence 271, Appl
Sequence 124, Appl
Sequence 38, Appl
Sequence 125, App
Sequence 6417, Ap
Sequence 4, Appl
Sequence 3, Appl
Sequence 2169, Ap
Sequence 19, Appl
Sequence 45875, A
Sequence 9, Appl
Sequence 272, App
Sequence 132351,
Sequence 230158,
Sequence 1713, Ap
Sequence 15, Appl
Sequence 36762, A
Sequence 49933, A
Sequence 51710,
Sequence 51762, A
Sequence 145076,
Sequence 204232,
Sequence 37241, A

330 9 US-09-925-299-876
330 10 US-09-925-299-876
484 13 US-10-092-063-27
484 14 US-10-286-926-27
484 15 US-10-231-913-123
467 15 US-10-231-913-36
379 15 US-10-231-913-271
484 15 US-10-231-913-124
446 15 US-10-231-913-38
455 15 US-10-231-913-125
479 15 US-10-369-433-6447
476 9 US-09-835-147-4
476 9 US-09-835-147-3
556 15 US-10-369-493-2169
467 9 US-09-129-112-19
467 12 US-10-425-114-45875
459 9 US-09-129-112-9
410 15 US-10-231-913-272
534 16 US-10-437-963-132351
467 12 US-10-424-599-230158
462 9 US-09-129-112-2
518 15 US-10-369-493-1713
462 9 US-09-129-112-15
433 12 US-10-425-114-36762
472 16 US-10-437-963-151710
457 12 US-10-425-114-51762
459 12 US-10-424-599-145076
449 16 US-10-437-963-204232
465 12 US-10-425-114-37241

ALIGNMENTS

RESULT 1

US-10-091-085-7
; Sequence 7, Application US/10091085
; Publication No. US20020146772A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/35761
; CURRENT APPLICATION NUMBER: US/10/091,085
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-091-085-7

Query Match 100.0%; Score 2252; DB 13; Length 428;
Best Local Similarity 100.0%; Pred. No. 3.7e-218;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MATSWGTFFFLVSVCSA VSHRQQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
1 MATSWGTFFFLVSVCSA VSHRQQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60

QY 61 RIHVYTFVQKMPGQQLPILGEVFDVSKPGLSAFVDQPKQAGTVOGLLEVAKDSIPRSHW 120
DB 61 RIHVYTFVQKMPGQQLPILGEVFDVSKPGLSAFVDQPKQAGTVOGLLEVAKDSIPRSHW 120
QY 121 KKTPTVLKATAGLRLLPEHKAKALLFEVKIEIFRKSPLVLPKGSVSIITQDEGFI PAWTV 180
DB 121 KKTPTVLKATAGLRLLPEHKAKALLFEVKIEIFRKSPLVLPKGSVSIITQDEGFI PAWTV 180
QY 181 NFLTQGLHGRHOETVGTDLGGASTQITFLPQFETLBOTPRGYLTSFEMFNSTYKLYTH 240
DB 181 NFLTQGLHGRHOETVGTDLGGASTQITFLPQFETLBOTPRGYLTSFEMFNSTYKLYTH 240
QY 241 SYLGFGLKAARLATIAGALETEGTDGHTFRSACLPRWLEAEWIFGCVKYQYGGNQEVEVP 300
DB 241 SYLGFGLKAARLATIAGALETEGTDGHTFRSACLPRWLEAEWIFGCVKYQYGGNQEVEVP 300
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DB 301 EPCYAEVLVRVVRKQLHQPVEVQSGSFYAFSYVYDRAVDTMDIDYKGGILKVEDFERKAR 360
QY 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQLTKKVNNIETGALGATFHL 420
DB 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQLTKKVNNIETGALGATFHL 420
QY 421 LOSLGISH 428
DB 421 LOSLGISH 428

RESULT 2

US-10-092-063-7
; Sequence 7, Application US/10092063
; Publication No. US20020173005A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
; FILE REFERENCE: 28110/35908
; CURRENT APPLICATION NUMBER: US/10/092,063
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-063-7

Query Match 100.0%; Score 2252; DB 13; Length 428;
Best Local Similarity 100.0%; Pred. No. 3.7e-218;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATSWGTVPFVPMVVCVCSAVSHRNQQTWTFEGIFLSSMCPINVSASTLYGIMFAGSTGT 60
DB 1 MATSWGTVPFVPMVVCVCSAVSHRNQQTWTFEGIFLSSMCPINVSASTLYGIMFAGSTGT 60
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DB 421 LOSLGISH 428

RESULT 3

US-10-286-926-7
; Sequence 7, Application US/10286926
; Publication No. US20030175752A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; FILE REFERENCE: 28110/36457CON
; CURRENT APPLICATION NUMBER: US/10/286,926
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-926-7

Query Match 100.0%; Score 2252; DB 14; Length 428;
Best Local Similarity 100.0%; Pred. No. 3.7e-218;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MATSWGTVPFVPMVVCVCSAVSHRNQQTWTFEGIFLSSMCPINVSASTLYGIMFAGSTGT 60

QY 61 RIHVYTFVQKMPGOLPILLEGVDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
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QY 121 KXTPVWLKATAGLRLLPEHKAALLFEVKIIFRKSPPFLVPKGSVSIIMGQDEGIFAWVTV 180
DB 121 KXTPVWLKATAGLRLLPEHKAALLFEVKIIFRKSPPFLVPKGSVSIIMGQDEGIFAWVTV 180
QY 181 NFLTGQHGHRQETVGTDLGGASTQITFLPQPEKTLQOTPRGYLTSFEMNSYKLYTH 240
DB 181 NFLTGQHGHRQETVGTDLGGASTQITFLPQPEKTLQOTPRGYLTSFEMNSYKLYTH 240
QY 241 SYLGFGGLKAARLATLGALETGTDGHTFRSACLPRWLEAEWIFGGVYQYGGNQEGBVGF 300
DB 241 SYLGFGGLKAARLATLGALETGTDGHTFRSACLPRWLEAEWIFGGVYQYGGNQEGBVGF 300
QY 301 EPCYAEVLVRVGRKLGHPQEEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
DB 301 EPCYAEVLVRVGRKLGHPQEEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
QY 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQLTCKVNNIETGWAIGATPHL 420
DB 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQLTCKVNNIETGWAIGATPHL 420
QY 421 LQSLGISH 428
DB 421 LQSLGISH 428

RESULT 4

US-10-091-085-3
; Sequence 3, Application US/10091085
; Publication No. US20020146772A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/35761
; CURRENT APPLICATION NUMBER: US/10/091.085
; CURRENT FILING DATE: 2002-03-05
; PRIOR FILING DATE: 1999-07-09
; PRIOR FILING DATE: 1998-07-16
; PRIOR FILING DATE: 1998-07-24
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; TYPE: PRT
; LENGTH: 428
; ORGANISM: Homo sapiens
US-10-091-085-3

Query Match 99.2%; Score 2235; DB 13; Length 428;
Best Local Similarity 99.3%; Pred. No. 1.9e-216;
Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MATSWGTVFFMLVWSCVCSAVSHRNQOTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSWGTVFFMLVWSCVCSAVSHRNQOTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
QY 61 RIHVYTFVQKMPGOLPILLEGVDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
DB 61 RIHVYTFVQKMPGOLPILLEGVDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
QY 121 KXTPVWLKATAGLRLLPEHKAALLFEVKIIFRKSPPFLVPKGSVSIIMGQDEGIFAWVTV 180

DB 121 KXTPVWLKATAGLRLLPEHKAALLFEVKIIFRKSPPFLVPKGSVSIIMGQDEGILAWVTV 180
QY 181 NFLTGQHGHRQETVGTDLGGASTQITFLPQPEKTLQOTPRGYLTSFEMNSYKLYTH 240
DB 181 NFLTGQHGHRQETVGTDLGGASTQITFLPQPEKTLQOTPRGYLTSFEMNSYKLYTH 240
QY 241 SYLGFGGLKAARLATLGALETGTDGHTFRSACLPRWLEAEWIFGGVYQYGGNQEGBVGF 300
DB 241 SYLGFGGLKAARLATLGALETGTDGHTFRSACLPRWLEAEWIFGGVYQYGGNQEGBVGF 300
QY 301 EPCYAEVLVRVGRKLGHPQEEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
DB 301 EPCYAEVLVRVGRKLGHPQEEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
QY 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQLTCKVNNIETGWAIGATPHL 420
DB 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQLTCKVNNIETGWAIGATPHL 420
QY 421 LQSLGISH 428
DB 421 LQSLGISH 428

RESULT 5

US-10-091-085-5
; Sequence 5, Application US/10091085
; Publication No. US20020146772A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/35761
; CURRENT APPLICATION NUMBER: US/10/091.085
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-091-085-5

Query Match 99.2%; Score 2235; DB 13; Length 428;
Best Local Similarity 99.3%; Pred. No. 1.9e-216;
Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MATSWGTVFFMLVWSCVCSAVSHRNQOTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSWGTVFFMLVWSCVCSAVSHRNQOTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
QY 61 RIHVYTFVQKMPGOLPILLEGVDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
DB 61 RIHVYTFVQKMPGOLPILLEGVDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
QY 121 KXTPVWLKATAGLRLLPEHKAALLFEVKIIFRKSPPFLVPKGSVSIIMGQDEGIFAWVTV 180
DB 121 KXTPVWLKATAGLRLLPEHKAALLFEVKIIFRKSPPFLVPKGSVSIIMGQDEGILAWVTV 180
QY 181 NFLTGQHGHRQETVGTDLGGASTQITFLPQPEKTLQOTPRGYLTSFEMNSYKLYTH 240
DB 181 NFLTGQHGHRQETVGTDLGGASTQITFLPQPEKTLQOTPRGYLTSFEMNSYKLYTH 240

QY 241 SYLGFLKAARLATIAGLETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGVP 300
DB 241 SYLGFLKAARLATIAGLETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGVP 300
QY 301 EPCVAEVLVRVVRGKLGHPQEVQSGSFYAFSYYYDRAVDVTMDIYEKGGILKVEDFERKAR 360
DB 301 EPCVAEVLVRVVRGKLGHPQEVQSGSFYAFSYYYDRAVDVTMDIYEKGGILKVEDFERKAR 360
QY 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQLTKKVNNIETGVALGATFHL 420
DB 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQLTKKVNNIETGVALGATFHL 420
QY 421 LQSLGISH 428
DB 421 LQSLGISH 428

RESULT 6

US-10-092-063-3
; Sequence 3, Application US/10092063
; Publication No. US20020173005A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
; FILE REFERENCE: 28110/35908
; CURRENT APPLICATION NUMBER: US/10/092,063
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-063-3

Query Match 99.2%; Score 2235; DB 13; Length 428;
Best Local Similarity 99.3%; Pred. No. 1.9e-216;
Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MATSNGTVFFMLVVCVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSNGTVFFMLVVCVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
QY 61 RIHVYTFVQKPGQLPILGEVFDVSKPGLSAFVDOPKQGAETVQGLLEVAKDSIPRSHW 120
DB 61 RIHVYTFVQKPGQLPILGEVFDVSKPGLSAFVDOPKQGAETVQGLLEVAKDSIPRSHW 120
QY 121 KXTPVVLKATAGRLLPKHAALLFEVKEIPRKSPLVPKGSVIMTQDEGIFAWTV 180
DB 121 KXTPVVLKATAGRLLPKHAALLFEVKEIPRKSPLVPKGSVIMTQDEGIFAWTV 180
QY 181 NFLTQGLHGRQETVGTLDLGGASTQITFLPQFENTLEQTPRGYLTSEFMENSTYKLYTH 240
DB 181 NFLTQGLHGRQETVGTLDLGGASTQITFLPQFENTLEQTPRGYLTSEFMENSTYKLYTH 240
QY 241 SYLGFLKAARLATIAGLETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGVP 300
DB 241 SYLGFLKAARLATIAGLETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGVP 300

QY 301 EPCVAEVLVRVVRGKLGHPQEVQSGSFYAFSYYYDRAVDVTMDIYEKGGILKVEDFERKAR 360
DB 301 EPCVAEVLVRVVRGKLGHPQEVQSGSFYAFSYYYDRAVDVTMDIYEKGGILKVEDFERKAR 360
QY 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQLTKKVNNIETGVALGATFHL 420
DB 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQLTKKVNNIETGVALGATFHL 420
QY 421 LQSLGISH 428
DB 421 LQSLGISH 428

RESULT 7

US-10-092-063-5
; Sequence 5, Application US/10092063
; Publication No. US20020173005A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
; FILE REFERENCE: 28110/35908
; CURRENT APPLICATION NUMBER: US/10/092,063
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-063-5

Query Match 99.2%; Score 2235; DB 13; Length 428;
Best Local Similarity 99.3%; Pred. No. 1.9e-216;
Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MATSNGTVFFMLVVCVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSNGTVFFMLVVCVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
QY 61 RIHVYTFVQKPGQLPILGEVFDVSKPGLSAFVDOPKQGAETVQGLLEVAKDSIPRSHW 120
DB 61 RIHVYTFVQKPGQLPILGEVFDVSKPGLSAFVDOPKQGAETVQGLLEVAKDSIPRSHW 120
QY 121 KXTPVVLKATAGRLLPKHAALLFEVKEIPRKSPLVPKGSVIMTQDEGIFAWTV 180
DB 121 KXTPVVLKATAGRLLPKHAALLFEVKEIPRKSPLVPKGSVIMTQDEGIFAWTV 180
QY 181 NFLTQGLHGRQETVGTLDLGGASTQITFLPQFENTLEQTPRGYLTSEFMENSTYKLYTH 240
DB 181 NFLTQGLHGRQETVGTLDLGGASTQITFLPQFENTLEQTPRGYLTSEFMENSTYKLYTH 240
QY 241 SYLGFLKAARLATIAGLETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGVP 300
DB 241 SYLGFLKAARLATIAGLETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGVP 300
QY 301 EPCVAEVLVRVVRGKLGHPQEVQSGSFYAFSYYYDRAVDVTMDIYEKGGILKVEDFERKAR 360
DB 301 EPCVAEVLVRVVRGKLGHPQEVQSGSFYAFSYYYDRAVDVTMDIYEKGGILKVEDFERKAR 360

Db 301 EPCYAEVLVVRGKHLQPEVQSGFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
Qy 361 EVCNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQTKKNNIETGHALGATPHL 420
Db 361 EVCNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQTKKNNIETGHALGATPHL 420
Qy 421 LOSLGISH 428
Db 421 LOSLGISH 428

RESULT 8
US-10-286-926-3
; Sequence 3, Application US/10286926
; Publication No. US20030175752A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; FILE REFERENCE: 28110/36457CON
; CURRENT APPLICATION NUMBER: US/10/286,926
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; TYPE: PRT
; LENGTH: 428
; ORGANISM: Homo sapiens
US-10-286-926-3

Query Match 99.2%; Score 2235; DB 14; Length 428;
Best Local Similarity 99.3%; Pred. No. 1.9e-216;
Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MATSWGTVFPMVLVVCSCVSAVSHRNQQTWFEGLFLSSMCPINVSASTLYGIMFDAGSTGT 60
Db 1 MATSWGTVFPMVLVVCSCVSAVSHRNQQTWFEGLFLSSMCPINVSASTLYGIMFDAGSTGT 60
Qy 61 RIHYVTVFQKMPGQLPILGEVFDVSKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
Db 61 RIHYVTVFQKMPGQLPILGEVFDVSKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
Qy 121 KKTPEVVLKATAGLRLPEHAKALLFEVKIIFRKSPLVPKGSVSIWGTGDEGIFAWTV 180
Db 121 KKTPEVVLKATAGLRLPEHAKALLFEVKIIFRKSPLVPKGSVSIWGTGDEGILAWTV 180
Qy 181 NFLTGQLHGRQETVGTLDLGASTQITFLPQFEKTLQTPRGYLTSPFEMNSTYKLYTH 240
Db 181 NFLTGQLHGRQETVGTLDLGASTQITFLPQFEKTLQTPRGYLTSPFEMNSTYKLYTH 240
Qy 241 SYLGFGLKAARLATLGALETGCTDGTFRSACLPRWLEAWIFGVKYQYGGNQEVEGV 300
Db 241 SYLGFGLKAARLATLGALETGCTDGTFRSACLPRWLEAWIFGVKYQYGGNQEVEGV 300

Qy 301 EPCYAEVLVVRGKHLQPEVQSGFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
Db 301 EPCYAEVLVVRGKHLQPEVQSGFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
Qy 361 EVCNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQTKKNNIETGHALGATPHL 420
Db 361 EVCNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQTKKNNIETGHALGATPHL 420
Qy 421 LOSLGISH 428
Db 421 LOSLGISH 428

RESULT 9
US-10-286-926-5
; Sequence 5, Application US/10286926
; Publication No. US20030175752A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; FILE REFERENCE: 28110/36457CON
; CURRENT APPLICATION NUMBER: US/10/286,926
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-926-5

Query Match 99.2%; Score 2235; DB 14; Length 428;
Best Local Similarity 99.3%; Pred. No. 1.9e-216;
Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MATSWGTVFPMVLVVCSCVSAVSHRNQQTWFEGLFLSSMCPINVSASTLYGIMFDAGSTGT 60
Db 1 MATSWGTVFPMVLVVCSCVSAVSHRNQQTWFEGLFLSSMCPINVSASTLYGIMFDAGSTGT 60
Qy 61 RIHYVTVFQKMPGQLPILGEVFDVSKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
Db 61 RIHYVTVFQKMPGQLPILGEVFDVSKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
Qy 121 KKTPEVVLKATAGLRLPEHAKALLFEVKIIFRKSPLVPKGSVSIWGTGDEGIFAWTV 180
Db 121 KKTPEVVLKATAGLRLPEHAKALLFEVKIIFRKSPLVPKGSVSIWGTGDEGILAWTV 180
Qy 181 NFLTGQLHGRQETVGTLDLGASTQITFLPQFEKTLQTPRGYLTSPFEMNSTYKLYTH 240
Db 181 NFLTGQLHGRQETVGTLDLGASTQITFLPQFEKTLQTPRGYLTSPFEMNSTYKLYTH 240

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Qy 241 SYLGFLKAARLATLGALETGTGHTFRSACLPRLWEAEWIFGGVKYQYGGNQEVEVF 300
Db 241 SYLGFLKAARLATLGALETGTGHTFRSACLPRLWEAEWIFGGVKYQYGGNQEVEVF 300
Qy 301 EPCYAEVLVRVGRKLPSEVQVGSFYAFSYDDRAVDTKMDYKGGILKVEDFERKAR 360
Db 301 EPCYAEVLVRVGRKLPSEVQVGSFYAFSYDDRAVDTKMDYKGGILKVEDFERKAR 360
Qy 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQTLTKKNNIETGWAIGATFHL 420
Db 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQTLTKKNNIETGWAIGATFHL 420
Qy 421 LQSLGISH 428
Db 421 LQSLGISH 428

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RESULT 10
US-10-231-913-127

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; Sequence 127, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia S.
; APPLICANT: Li, Li
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyackar, Uriel M.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.
; APPLICANT: Spytex, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Edinger, Schlomit
; APPLICANT: Peyman, John A.
; APPLICANT: Stone, David J.
; APPLICANT: Ellerman, Karen
; APPLICANT: Gangolli, Ssha A.
; APPLICANT: Boldog, Ference L.
; APPLICANT: Colman, Steven D.
; APPLICANT: Eisen, Andrew J.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-216
; CURRENT APPLICATION NUMBER: US/10/231,913
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/251,660
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/255,029
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/260,326
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/263,800
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/269,942
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/286,183
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/313,627
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/318,712
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 127
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-231-913-127

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Query Match 99.2%; Score 2235; DB 15; Length 428;
Best Local Similarity 99.3%; Pred. No. 1.9e-216; Indels 0; Gaps 0;
Matches 425; Conservative 0; Mismatches 3;
Qy 1 MATSWGTVFVFLVVCVCSAVSHRNQQTWFEIGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
Db 1 MATSWGTVFVFLVVCVCSAVSHRNQQTWFEIGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
Qy 61 RIHYVTFVQKMPQQLPILGEVDFSVKPGLSAFVDPKQGAETVQGLLEVAKDISIPRSHW 120
Db 61 RIHYVTFVQKMPQQLPILGEVDFSVKPGLSAFVDPKQGAETVQGLLEVAKDISIPRSHW 120
Qy 121 KKTPTVVKATAGLRLLPEHKAKALLFEVKSIIRKSPFLVFKGVSIMDGSDEGILLAWTV 180
Db 121 KKTPTVVKATAGLRLLPEHKAKALLFEVKSIIRKSPFLVFKGVSIMDGSDEGILLAWTV 180
Qy 181 NELTGOLHGHROBTVTGTLGGASTQITFLPQFKTELEQTPRGYLTSEFENSTYKLYTH 240
Db 181 NELTGOLHGHROBTVTGTLGGASTQITFLPQFKTELEQTPRGYLTSEFENSTYKLYTH 240
Qy 241 SYLGFLKAARLATLGALETGTGHTFRSACLPRLWEAEWIFGGVKYQYGGNQEVEVF 300
Db 241 SYLGFLKAARLATLGALETGTGHTFRSACLPRLWEAEWIFGGVKYQYGGNQEVEVF 300
Qy 301 EPCYAEVLVRVGRKLPSEVQVGSFYAFSYDDRAVDTKMDYKGGILKVEDFERKAR 360
Db 301 EPCYAEVLVRVGRKLPSEVQVGSFYAFSYDDRAVDTKMDYKGGILKVEDFERKAR 360
Qy 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQTLTKKNNIETGWAIGATFHL 420
Db 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQTLTKKNNIETGWAIGATFHL 420
Qy 421 LQSLGISH 428
Db 421 LQSLGISH 428

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RESULT 11

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US-10-408-765A-2296
; Sequence 2296, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Boim D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2296
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2296

```

```

Query Match 98.6%; Score 2221; DB 16; Length 428;
Best Local Similarity 98.8%; Pred. No. 5e-215; Indels 0; Gaps 0;
Matches 423; Conservative 0; Mismatches 5;
Qy 1 MATSWGTVFVFLVVCVCSAVSHRNQQTWFEIGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
Db 1 MATSWGTVFVFLVVCVCSAVSHRNQQTWFEIGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
Qy 61 RIHYVTFVQKMPQQLPILGEVDFSVKPGLSAFVDPKQGAETVQGLLEVAKDISIPRSHW 120
Db 61 RIHYVTFVQKMPQQLPILGEVDFSVKPGLSAFVDPKQGAETVQGLLEVAKDISIPRSHW 120

```

121 KKTPTVLKATAGLRLPEHAKALLFEVKEI FRKSPFLVPKGSVSIMTGDGEGIFAWTV 180
 121 NFLTQGLHGRQETVGTLDGGASTQITFLPOFEKTLQTPRGVLTSPFEMNSTYKLYTH 240
 121 KKTPTVLKATAGLRLPEHAKALLFEVKEI FRKSPFLVPKGSVSIMTGDGEGIFAWTV 180
 181 NFLTQGLHGRQETVGTLDGGASTQITFLPOFEKTLQTPRGVLTSPFEMNSTYKLYTH 240
 181 NFLTQGLHGRQETVGTLDGGASTQITFLPOFEKTLQTPRGVLTSPFEMNSTYKLYTH 240
 241 SYLGFGGLKAARLALATLGALETGTGHTFRSACLPRWLEAEWIFGGVYKYQYGGNQEGBVGF 300
 241 SYLGFGGLKAARLALATLGALETGTGHTFRSACLPRWLEAEWIFGGVYKYQYGGNQEGBVGF 300
 301 EPCYAEVLVRVRGKQHQPVEVQSGSFYAFSYYYDRAVDTMIDYEKGGLKVEDFERKAR 360
 301 EPCYAEVLVRVRGKQHQPVEVQSGSFYAFSYYYDRAVDTMIDYEKGGLKVEDFERKAR 360
 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQTKKVNNIETGALGATFHL 420
 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQTKKVNNIETGALGATFHL 420
 421 LOSLGISH 428
 421 LOSLGISH 428

RESULT 12
 ; Sequence 25, Application US/10092063
 ; Publication No. US20020173005A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ford, John
 ; APPLICANT: Mulero, Julio
 ; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
 ; FILE REFERENCE: 28110/35908
 ; CURRENT APPLICATION NUMBER: US/10/092,063
 ; PRIOR FILING DATE: 2002-03-05
 ; PRIOR APPLICATION NUMBER: 09/370,265
 ; PRIOR FILING DATE: 2002-01-31
 ; PRIOR APPLICATION NUMBER: PCT/US99/16180
 ; PRIOR FILING DATE: 1999-07-15
 ; PRIOR APPLICATION NUMBER: 09/350,836
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: 09/273,447
 ; PRIOR FILING DATE: 1999-03-19
 ; PRIOR APPLICATION NUMBER: 09/244,444
 ; PRIOR FILING DATE: 1999-02-04
 ; PRIOR APPLICATION NUMBER: 09/122,449
 ; PRIOR FILING DATE: 1998-07-24
 ; PRIOR APPLICATION NUMBER: 09/118,205
 ; PRIOR FILING DATE: 1998-07-16
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 25
 ; LENGTH: 405
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-092-063-25

Query Match 92.8%; Score 2089; DB 13; Length 405;
 Best Local Similarity 99.2%; Pred. No. 9.7e-202;
 Matches 397; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MATSNGTVFFMLVWSCVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
 DB 1 MATSNGTVFFMLVWSCVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
 QY 61 RIHYVTFVQKMPGQLPILEGVEFDSVKPGLSAFVDPQKGAETVQGLLEVAKDSIPRSHW 120
 DB 61 RIHYVTFVQKMPGQLPILEGVEFDSVKPGLSAFVDPQKGAETVQGLLEVAKDSIPRSHW 120
 QY 121 KKTPTVLKATAGLRLPEHAKALLFEVKEI FRKSPFLVPKGSVSIMTGDGEGIFAWTV 180

121 KKTPTVLKATAGLRLPEHAKALLFEVKEI FRKSPFLVPKGSVSIMTGDGEGIFAWTV 180
 181 NFLTQGLHGRQETVGTLDGGASTQITFLPOFEKTLQTPRGVLTSPFEMNSTYKLYTH 240
 181 NFLTQGLHGRQETVGTLDGGASTQITFLPOFEKTLQTPRGVLTSPFEMNSTYKLYTH 240
 241 SYLGFGGLKAARLALATLGALETGTGHTFRSACLPRWLEAEWIFGGVYKYQYGGNQEGBVGF 300
 241 SYLGFGGLKAARLALATLGALETGTGHTFRSACLPRWLEAEWIFGGVYKYQYGGNQEGBVGF 300
 301 EPCYAEVLVRVRGKQHQPVEVQSGSFYAFSYYYDRAVDTMIDYEKGGLKVEDFERKAR 360
 301 EPCYAEVLVRVRGKQHQPVEVQSGSFYAFSYYYDRAVDTMIDYEKGGLKVEDFERKAR 360
 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQ 400
 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQ 400

RESULT 13
 ; Sequence 25, Application US/10286926
 ; Publication No. US20030175752A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ford, John
 ; APPLICANT: Mulero, Julio
 ; APPLICANT: Yeung, George
 ; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
 ; FILE REFERENCE: 28110/36457CON
 ; CURRENT APPLICATION NUMBER: US/10/286,926
 ; PRIOR FILING DATE: 2002-11-01
 ; PRIOR APPLICATION NUMBER: 09/557,800
 ; PRIOR FILING DATE: 2000-04-25
 ; PRIOR APPLICATION NUMBER: 09/481,238
 ; PRIOR FILING DATE: 2000-01-11
 ; PRIOR APPLICATION NUMBER: 09/370,265
 ; PRIOR FILING DATE: 1999-08-09
 ; PRIOR APPLICATION NUMBER: PCT/US99/16180
 ; PRIOR FILING DATE: 1999-07-16
 ; PRIOR APPLICATION NUMBER: 09/350836
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: 09/273447
 ; PRIOR FILING DATE: 1999-03-19
 ; PRIOR APPLICATION NUMBER: 09/122449
 ; PRIOR FILING DATE: 1998-07-24
 ; PRIOR APPLICATION NUMBER: 09/244444
 ; PRIOR FILING DATE: 1999-02-04
 ; PRIOR APPLICATION NUMBER: 09/118,205
 ; PRIOR FILING DATE: 1998-07-16
 ; NUMBER OF SEQ ID NOS: 54
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 25
 ; LENGTH: 405
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-286-926-25

Query Match 92.8%; Score 2089; DB 14; Length 405;
 Best Local Similarity 99.2%; Pred. No. 9.7e-202;
 Matches 397; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MATSNGTVFFMLVWSCVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
 DB 1 MATSNGTVFFMLVWSCVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
 QY 61 RIHYVTFVQKMPGQLPILEGVEFDSVKPGLSAFVDPQKGAETVQGLLEVAKDSIPRSHW 120
 DB 61 RIHYVTFVQKMPGQLPILEGVEFDSVKPGLSAFVDPQKGAETVQGLLEVAKDSIPRSHW 120
 QY 121 KKTPTVLKATAGLRLPEHAKALLFEVKEI FRKSPFLVPKGSVSIMTGDGEGIFAWTV 180
 DB 121 KKTPTVLKATAGLRLPEHAKALLFEVKEI FRKSPFLVPKGSVSIMTGDGEGIFAWTV 180

QY 181 NLTGQLHGRQETVGTDLGGASTQITFLPQPEKTLQTPRGVLTSTFEMFNSTYKLYTH 240
 DB 181 NLTGQLHGRQETVGTDLGGASTQITFLPQPEKTLQTPRGVLTSTFEMFNSTYKLYTH 240
 QY 241 SYLGGLKKAARLATLGALETGTGHTTFRSACLPRWLEAEI FGVKYQYGGNQBGEVGF 300
 DB 241 SYLGGLKKAARLATLGALETGTGHTTFRSACLPRWLEAEI FGVKYQYGGNQBGEVGF 300
 QY 301 EPCYAEVLVRVGRKHLQPEEVQVGSFYAFSYYYDRADVDTMDIYEKGGILKVEDFERKAR 360
 DB 301 EPCYAEVLVRVGRKHLQPEEVQVGSFYAFSYYYDRADVDTMDIYEKGGILKVEDFERKAR 360
 QY 361 EVCNDNLTSSPFLCMLDLSYITALLKDGFGFADSTVLQ 400
 DB 361 EVCNDNLTSSPFLCMLDLSYITALLKDGFGFADSTVLQ 400

RESULT 14
 US-10-231-913-126
 ; Sequence 126, Application US/10231913
 ; Publication No. US20040005576A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Guo, Xiaojia S.
 ; APPLICANT: Li, Li
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Shimkets, Richard A.
 ; APPLICANT: Casman, Stacie J.
 ; APPLICANT: Malyankar, Uriel M.
 ; APPLICANT: Tchernev, Velizar T.
 ; APPLICANT: Vernet, Corine A.
 ; APPLICANT: Spytek, Kimberly A.
 ; APPLICANT: Shenoy, Suresh G.
 ; APPLICANT: Alsobrook II, John P.
 ; APPLICANT: Edinger, Schlomit
 ; APPLICANT: Peyman, John A.
 ; APPLICANT: Stone, David J.
 ; APPLICANT: Ellerman, Karen
 ; APPLICANT: Gangolli, Esha A.
 ; APPLICANT: Boldog, Ference L.
 ; APPLICANT: Colman, Steven D.
 ; APPLICANT: Eisen, Andrew J.
 ; APPLICANT: Liu, Xiaohong
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Spaderna, Steven K.
 ; APPLICANT: Zehnusen, Bryan D.

; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 21402-216
 ; CURRENT APPLICATION NUMBER: US/10/231,913
 ; PRIOR FILING DATE: 2002-08-30
 ; PRIOR APPLICATION NUMBER: 60/251,660
 ; PRIOR FILING DATE: 2000-12-06
 ; PRIOR APPLICATION NUMBER: 60/255,029
 ; PRIOR FILING DATE: 2000-12-12
 ; PRIOR APPLICATION NUMBER: 60/260,326
 ; PRIOR FILING DATE: 2001-01-08
 ; PRIOR APPLICATION NUMBER: 60/263,800
 ; PRIOR FILING DATE: 2001-01-24
 ; PRIOR APPLICATION NUMBER: 60/269,942
 ; PRIOR FILING DATE: 2001-02-20
 ; PRIOR APPLICATION NUMBER: 60/286,183
 ; PRIOR FILING DATE: 2001-04-24
 ; PRIOR APPLICATION NUMBER: 60/313,627
 ; PRIOR FILING DATE: 2001-08-20
 ; PRIOR APPLICATION NUMBER: 60/318,712
 ; PRIOR FILING DATE: 2001-09-12
 ; NUMBER OF SEQ ID NOS: 292
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 126
 ; LENGTH: 427
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-231-913-126

Query Match 80.9%; Score 1822.5; DB 13; Length 465;
 Best Local Similarity 83.3%; Pred. No. 9.7e-175;

Query Match 87.9%; Score 1979.5; DB 15; Length 427;
 Best Local Similarity 87.6%; Pred. No. 1.2e-190;
 Matches 374; Conservative 24; Mismatches 28; Indels 1; Gaps 1;
 QY 1 MATSWGTVFPMLVVSCVSAVSHRNOQTWPEGIPLSSMCPINVSASTLYGIMFDAGSTGT 60
 DB 1 MATSWGAV-PMIIACUGSTVVFYREQQTWPEGVFLSSMCPINVSAGTFYGIMFDAGSTGT 59
 QY 61 RIHYTFVQMPQOLPILGEVFDVSKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
 DB 60 RIHYTFVQKTAGQLPPEGEIFDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 119
 QY 121 KKTPTVVLKATAGLRLPEHKAKALLEVEKEI FRKSPFLVPKGSVSIWTCODEGIPKAVTV 180
 DB 120 ERTPTVVLKATAGLRLPEKQKALLLEVEEIFKNSPFLVPDGSVSIWMDGSYEGILAWTV 179
 QY 181 NLTGQLHGRQETVGTDLGGASTQITFLPQPEKTLQTPRGVLTSTFEMFNSTYKLYTH 240
 DB 180 NLTGQLHGRQETVGTDLGGASTQITFLPQPEKTLQTPRGVLTSTFEMFNSTYKLYTH 239
 QY 241 SYLGGLKKAARLATLGALETGTGHTTFRSACLPRWLEAEI FGVKYQYGGNQBGEVGF 300
 DB 240 SYLGGLKKAARLATLGALETGTGHTTFRSACLPRWLEAEI FGVKYQYGGNQBGEVGF 299
 QY 301 EPCYAEVLVRVGRKHLQPEEVQVGSFYAFSYYYDRADVDTMDIYEKGGILKVEDFERKAR 360
 DB 300 EPCYAEVLVRVGRKHLQPEEVQVGSFYAFSYYYDRADVDTMDIYEKGGILKVEDFERKAR 359
 QY 361 EVCNDNLTSSPFLCMLDLSYITALLKDGFGFADSTVLQTKKVNITGVALGATPHL 420
 DB 360 EVCNDNLTSSPFLCMLDLYITALLKDGFGFADGTLQLTKKVNITGVALGATPHL 419
 QY 421 LQSLGITS 427
 DB 420 LQSLGIT 426

RESULT 15
 US-10-092-063-39
 ; Sequence 39, Application US/10092063
 ; Publication No. US20020173005A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ford, John
 ; APPLICANT: Mulero, Julio
 ; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDE
 ; FILE REFERENCE: 28110/35908
 ; CURRENT APPLICATION NUMBER: US/10/092,063
 ; CURRENT FILING DATE: 2002-03-05
 ; PRIOR FILING DATE: 2002-01-31
 ; PRIOR APPLICATION NUMBER: PCT/US99/16180
 ; PRIOR FILING DATE: 1999-07-16
 ; PRIOR APPLICATION NUMBER: 09/350,836
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: 09/273,447
 ; PRIOR FILING DATE: 1999-03-19
 ; PRIOR APPLICATION NUMBER: 09/244,444
 ; PRIOR FILING DATE: 1999-02-04
 ; PRIOR APPLICATION NUMBER: 09/122,449
 ; PRIOR FILING DATE: 1998-07-24
 ; PRIOR APPLICATION NUMBER: 09/118,205
 ; PRIOR FILING DATE: 1998-07-16
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 39
 ; LENGTH: 465
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-092-063-39

Query Match 80.9%; Score 1822.5; DB 13; Length 465;
 Best Local Similarity 83.3%; Pred. No. 9.7e-175;

Search completed: July 1, 2004, 13:58:41
Job time : 45.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 1, 2004, 13:41:36 ; Search time 52 Seconds
(without alignments)
2325.583 Million cell updates/sec

Title: US-10-091-085-7

Perfect score: 2252

Sequence: 1 MATSWGVRFFMLVVCVCSA.....ETGWALGATPHLLQSLGISH 428

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_29Jan04.*

- 1: Geneseq_1980s.*
- 2: Geneseq_1990s.*
- 3: Geneseq_2000s.*
- 4: Geneseq_2001s.*
- 5: Geneseq_2002s.*
- 6: Geneseq_2003as.*
- 7: Geneseq_2003bs.*
- 8: Geneseq_2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2252	100.0	428	3 AAY44850	Aay44850 Human CD3
2	2252	100.0	428	4 AAB72240	Aab72240 Human CD3
3	2235	99.2	428	3 AAY44849	Aay44849 Human CD3
4	2235	99.2	428	4 AAB72238	Aab72238 Human CD3
5	2235	99.2	428	4 AAB72243	Aab72243 Human CD3
6	2235	99.2	428	5 AAE19883	Aae19883 Human CD3
7	2089	92.8	405	3 AAY44851	Aay44851 Human CD3
8	2089	92.8	405	4 AAB72239	Aab72239 Human CD3
9	1817.5	80.7	465	5 AAE19884	Aae19884 Mouse CD3
10	1645	73.0	330	3 AAB53336	Aab53336 Human col
11	996	44.2	456	5 AAE19881	Aae19881 Human CD3
12	996	44.2	484	4 AAB72241	Aab72241 Human CD3
13	993	44.1	463	5 ABB06124	Abb06124 Human NS
14	993	44.1	467	5 ABL04657	Abj04657 Protein o
15	989	43.9	456	4 AAM93929	Aam93929 Human pol
16	986	43.8	446	5 AAB70458	Abj04658 Protein o
17	938	41.7	450	7 ADC14220	Adc14220 Human enz
18	894	39.7	462	4 AAU30882	Aau30882 Novel hum
19	816.5	36.3	471	4 AAB72242	Aab72242 Mature hu
20	693.5	30.8	461	4 ABB66213	Abb66213 Drosophil
21	693.5	30.8	464	4 ABB59611	Abb59611 Drosophil
22	605	26.9	476	3 AAY70912	Aay70912 Human CD3
23	605	26.9	476	3 AAY70889	Aay70889 Protein e
24	548	24.3	476	3 AAY70911	Aay70911 Human CD3
25	548	24.3	476	3 AAY70888	Aay70888 Protein e

ALIGNMENTS

RESULT 1

AAY44850

ID AAY44850 standard; protein; 428 AA.

XX AAY44850;

AC AC (first entry)

DT 18-MAY-2000

XX Human CD39-L4 variant-ACR III mutant protein.

DE Human CD39-L4; human; apyrase; nucleotide diphosphatase; NDPase; variant;

KW ATP diphosphohydrolase; ATPase; adenosine diphosphate; ADP; treatment;
KW platelet aggregation; antithrombotic; thrombosis; myocardial infarction;
KW cerebral ischemia; angina; vascular graft; extracorporeal circulation;
KW molecular weight marker; nutritional supplement; tumour; prevention;
KW drug targeting; substitution mutation.
XX Homo sapiens.
OS Synthetic.

PH Key Location/Qualifiers

FT Misc-difference 168 /note= "wild type Asp substituted with Thr"

FT Misc-difference 170 /note= "wild type Ser substituted with Gln"

FT Misc-difference 175 /note= "wild type Leu substituted with Phe"

XX WO200004041-A2.

PD 27-JAN-2000.

XX 16-JUL-1999; 99WO-US016180.

XX 16-JUL-1998; 98US-00118205.

XX 24-JUL-1998; 98US-00122449.

XX 04-FEB-1999; 99US-00244444.

XX 19-MAR-1999; 99US-00273447.

XX 09-JUL-1999; 99US-00350836.

XX (HYSE-) HYSEQ INC.

XX Ford J, Mulero J;

XX WPI; 2000-182397/16.

XX N-PSDS; AAZ50357.

XX New nucleic acid encoding human CD39-like protein, useful for treating

PT and preventing thrombotic disease.

PS Claim 17; Fig 6; 125pp; English.

XX The present amino acid sequence is the CD39-L4 variant, designated as ACR
CC III mutant protein, an apyrase and/or nucleotide diphosphatase (NDPase).
CC It is isolated from the human foetal liver spleen cDNA library,
CC b2HPLS20W. It is a soluble ATP diphosphohydrolases (ATPase) and is
CC involved in the hydrolysis of adenosine diphosphate (ADP), the agonist
CC that causes platelet aggregation. CD39-L4 protein has 30% and 80%
CC homology to human and murine CD39. It has platelet aggregation inhibition
CC and antithrombotic activity. CD39-L4 is used to treat or prevent
CC thrombosis, myocardial infarction, cerebral ischaemia and angina. It is
CC also used in vitro, to maintain vascular grafts or during extracorporeal
CC circulation, to hydrolyse NDP, as molecular weight markers and as
CC nutritional supplements. It is used to identify therapeutic agents that
CC bind and modulate CD39-L4. It is coupled to toxins for targeting drugs to
CC tumours or other cells that express CD39-L4

XX Sequence 428 AA;

Query Match 100.0%; Score 2252; DB 3; Length 428;

Best Local Similarity 100.0%; Pred. No. 9e-209;

Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATSGTFFVFNLVVSCVSAVSHRNQQTWFEGLFSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSGTFFVFNLVVSCVSAVSHRNQQTWFEGLFSSMCPINVSASTLYGIMFDAGSTGT 60
QY 61 RIHWYTFVQKMPGQLPILLEGVFDVSKPGLSAFVDPKQGAETVQGLLEVAKDSIPRSHW 120
DB 61 RIHWYTFVQKMPGQLPILLEGVFDVSKPGLSAFVDPKQGAETVQGLLEVAKDSIPRSHW 120
QY 121 KKTIPVVKATAGLRLPEHKAKALLPEVKEIFRKSPFLVPKGSVIMTQDEGIFANVTV 180
DB 121 KKTIPVVKATAGLRLPEHKAKALLPEVKEIFRKSPFLVPKGSVIMTQDEGIFANVTV 180
QY 181 NFLTQGLHGHROETVGTLDLGGASTQITFLPQFEXTLEQTPRGYLTSEMFNSTYKLYTH 240
DB 181 NFLTQGLHGHROETVGTLDLGGASTQITFLPQFEXTLEQTPRGYLTSEMFNSTYKLYTH 240
QY 241 SYLGPLKAARLALGALTEGTGHTFRSACLPRWLEAEMIPGVKTYQYGNQEGEVGF 300
DB 241 SYLGPLKAARLALGALTEGTGHTFRSACLPRWLEAEMIPGVKTYQYGNQEGEVGF 300
QY 301 EPCYAEVLVRVKGKHOPEVORGSGFYAFSYVYDRAVDTMDIDYKGGILKVEBPERKAR 360
DB 301 EPCYAEVLVRVKGKHOPEVORGSGFYAFSYVYDRAVDTMDIDYKGGILKVEBPERKAR 360
QY 361 EVCNLENFTSGSPFLCWDLSYITALLKXGFGFADSTVLQLTQKVNNTETGALCATPHL 420
DB 361 EVCNLENFTSGSPFLCWDLSYITALLKXGFGFADSTVLQLTQKVNNTETGALCATPHL 420
QY 421 LOSLGISH 428
DB 421 LOSLGISH 428

RESULT 2

AAB72240

ID AAB72240 standard; protein; 428 AA.

XX AAB72240;

XX AAB72240;

DT 14-MAY-2001 (first entry)

XX Human CD39 like protein CD39-L4 variant ACRIII amino acid sequence.

XX Human CD39-like protein; apyrase; NDPase; platelet function inhibitor;
KW myocardial infarction; cerebral ischaemia; angina; arterial thrombosis;
KW cerebral artery thrombosis; platelet aggregation; inflammation;
KW apoptosis; autoimmune disorder; neurological disorder; mutant; mutein;
KW Alzheimer's disease; Parkinson's disease; cancer; CD39-L4.

XX Homo sapiens.
OS WC200110205-A1.
PN

XX 15-FEB-2001.

XX 09-AUG-2000; 2000WO-US021790.

XX 09-AUG-1999; 99US-00370265.

XX 11-JAN-2000; 2000US-00481238.

XX 25-APR-2000; 2000US-00557800.

XX 28-MAY-2000; 2000US-00582231.

XX 30-JUN-2000; 2000US-00608285.

XX (HYSE-) HYSEQ INC.

XX Ford J, Mulero JJ, Yeung G;

XX WPI; 2001-147489/15.

XX N-PSDB; AAF63385.

XX Polynucleotides encoding human CD39-like polypeptides, with apyrase

XX and/or NDPase activity, which are useful in the treatment of pathological

XX conditions caused by thrombosis (e.g. myocardial infarction) and

XX inflammatory disorders.

XX Claim 19; Fig 6; 203pp; English.

XX This invention relates to polynucleotides encoding human CD39-like

XX polypeptides with apyrase and/or NDPase activity. The polypeptides having

XX ATPase, including NDPase, activity are useful for inhibiting platelet

XX function and can therefore be used in the prophylaxis or treatment of

XX pathological conditions caused by or involving thrombosis or excessive

XX coagulation or excessive platelet aggregation, such as myocardial

XX infarction, cerebral ischaemia, angina, arterial thrombosis, cerebral

XX artery thrombosis or intracardiac thrombosis, and conditions associated

XX with venous thrombosis. CD39-L4 and CD39-L2 polypeptides are useful in

XX modulating disease states (including platelet aggregation, inflammation

XX and apoptosis) associated with ADP or other purinergic signalling by

XX reducing the levels of NDPs. The polypeptides are also useful for

XX prophylaxis or treatment of inflammation related disorders, such as

XX disorders involving sepsis or systemic inflammatory response syndrome or

XX SIRS (and associated conditions such as fever, tachycardia, tachypnea,

XX cytokine overstimulation); autoimmune disorders such as thrombosis,

XX atherosclerosis, acute pancreatitis, dermatitis, including psoriasis,

XX cirrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis,

XX neurological disorders including neurodegenerative diseases, epilepsy,

XX depression, Alzheimer's disease, Parkinson's disease, Huntington's

XX disease, and amyotrophic lateral sclerosis; and cancer. The present

XX sequence represents human CD39 like protein CD39-L4 variant ACRIII

XX Sequence 428 AA;

Query Match 100.0%; Score 2252; DB 4; Length 428;

Best Local Similarity 100.0%; Pred. No. 9e-209;

Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATSGTFFVFNLVVSCVSAVSHRNQQTWFEGLFSSMCPINVSASTLYGIMFDAGSTGT 60

DB 1 MATSGTFFVFNLVVSCVSAVSHRNQQTWFEGLFSSMCPINVSASTLYGIMFDAGSTGT 60

QY 61 RIHWYTFVQKMPGQLPILLEGVFDVSKPGLSAFVDPKQGAETVQGLLEVAKDSIPRSHW 120

DB 61 RIHWYTFVQKMPGQLPILLEGVFDVSKPGLSAFVDPKQGAETVQGLLEVAKDSIPRSHW 120

QY 121 KKTIPVVKATAGLRLPEHKAKALLPEVKEIFRKSPFLVPKGSVIMTQDEGIFANVTV 180

DB 121 KKTIPVVKATAGLRLPEHKAKALLPEVKEIFRKSPFLVPKGSVIMTQDEGIFANVTV 180

QY 181 NFLTQGLHGHROETVGTLDLGGASTQITFLPQFEXTLEQTPRGYLTSEMFNSTYKLYTH 240

DB 181 NFLTQGLHGHROETVGTLDLGGASTQITFLPQFEXTLEQTPRGYLTSEMFNSTYKLYTH 240

QY 241 SYLGFLGKAARLATLGALETGTGDTGHTFRSACLPRLMEAPWIFGGVKYQYGGNQEVEGVF 300
Db 241 SYLGFLGKAARLATLGALETGTGDTGHTFRSACLPRLMEAPWIFGGVKYQYGGNQEVEGVF 300
QY 301 EPCYAEVLVRVGRKLRHQPVEVQSGSFYAFSYVDRAVDMDIDYKGGILKVEDFERKAR 360
Db 301 EPCYAEVLVRVGRKLRHQPVEVQSGSFYAFSYVDRAVDMDIDYKGGILKVEDFERKAR 360
QY 361 EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQLTCKVNNIETGVALGATFHL 420
Db 361 EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQLTCKVNNIETGVALGATFHL 420
QY 421 LQSLGISH 428
Db 421 LQSLGISH 428

RESULT 3
AA44849
ID AAY44849 standard; protein; 428 AA.
AC AAY44849;
XX 18-MAY-2000 (first entry)
DT Human CD39-L4 protein.
DE
XX CD39-L4; human; apyrase; nucleotide diphosphatase; NDPase;
KW ATP diphosphohydrolase; ATPase; adenosine diphosphate; ADP; treatment;
KW platelet aggregation; antithrombotic; thrombosis; myocardial infarction;
KW cerebral ischaemia; angina; vascular graft; extracorporeal circulation;
KW molecular weight marker; nutritional supplement; tumour; prevention;
KW drug targeting; Apyrase Conserved Region; ACR.
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Peptide 1..22 /label= Leader_peptide
FT Protein 23..428 /label= Mature_human_CD39-L4_protein
FT /note= "Homologous to human and murine CD39"
FT Binding-site 54..58 /label= ATP_Binding_region
FT Region 129..134 /label= Apyrase_Conserved_Region
FT Region 169..173 /label= Apyrase_Conserved_Region
FT Region 199..206 /note= "Conserved motif in ATPases"
FT
XX WC200004041-A2.
PN
XX
XX 27-JAN-2000.
XX
XX 16-JUL-1999; 99WO-US016180.
XX
PR 16-JUL-1998; 98US-00118205.
PR 24-JUL-1998; 98US-00124439.
PR 04-FEB-1999; 99US-00244444.
PR 19-MAR-1999; 99US-00273447.
PR 09-JUL-1999; 99US-00350836.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Ford J, Mulero J;
XX
XX WPI; 2000-182397/16.
DR N-PSDB; AA250356; AA250359.
XX
XX New nucleic acid encoding human CD39-like protein, useful for treating
PT and preventing thrombotic disease.

XX Claim 15; Fig 2; 125pp; English.
PS The present amino acid sequence is the CD39-L4 protein, an apyrase and/or
XX nucleotide diphosphatase (NDPase). It is isolated from the human foetal
CC liver-spleen cDNA library, b2HPLS20W. It is a soluble ATP
CC diphosphohydrolase (ATPDase) and is involved in the hydrolysis of
CC adenosine diphosphate (ADP), the agonist that causes platelet
CC aggregation. CD39-L4 protein has 30% and 80% homology to human and murine
CC CD39. It has platelet aggregation inhibition and antithrombotic activity.
CC CD39-L4 is used to treat or prevent thrombosis, myocardial infarction,
CC cerebral ischaemia and angina. It is also used in vitro, to maintain
CC vascular grafts or during extracorporeal circulation, to hydrolyse NDP,
CC as molecular weight markers and as nutritional supplements. It is used to
CC identify therapeutic agents that bind and modulate CD39-L4. It is coupled
CC to toxins for targeting drugs to tumours or other cells that express CD39
XX -L4
XX
SQ Sequence 428 AA;
Query Match 99.2%; Score 2235; DB 3; Length 428;
Best Local Similarity 99.3%; Pred. No. 4e-207;
Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MATSWGTVFFMLVWSCVSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
Db 1 MATSWGTVFFMLVWSCVSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
QY 61 RIHVYTFQKMPGQPLILEGEVDSVKPGLSAFVDPKQGAFTVQGLLEVAKDSIPRSHW 120
Db 61 RIHVYTFQKMPGQPLILEGEVDSVKPGLSAFVDPKQGAFTVQGLLEVAKDSIPRSHW 120
QY 121 KKTVPVLKATAGLRLLPEKAKALLFEVKEIFPKSPFLVPKGSVIMTQDSEGIFAWVTV 180
Db 121 KKTVPVLKATAGLRLLPEKAKALLFEVKEIFPKSPFLVPKGSVIMTQDSEGIFAWVTV 180
QY 181 NFLTQQLHGHROETVGTLDLGGASTQITFLPQETKLSOTPRGYLTSPFEMFNSTYKLYTH 240
Db 181 NFLTQQLHGHROETVGTLDLGGASTQITFLPQETKLSOTPRGYLTSPFEMFNSTYKLYTH 240
QY 241 SYLGFLGKAARLATLGALETGTGHTFRSACLPRLMEAPWIFGGVKYQYGGNQEVEGVF 300
Db 241 SYLGFLGKAARLATLGALETGTGHTFRSACLPRLMEAPWIFGGVKYQYGGNQEVEGVF 300
QY 301 EPCYAEVLVRVGRKLRHQPVEVQSGSFYAFSYVDRAVDMDIDYKGGILKVEDFERKAR 360
Db 301 EPCYAEVLVRVGRKLRHQPVEVQSGSFYAFSYVDRAVDMDIDYKGGILKVEDFERKAR 360
QY 361 EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQLTCKVNNIETGVALGATFHL 420
Db 361 EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQLTCKVNNIETGVALGATFHL 420
QY 421 LQSLGISH 428
Db 421 LQSLGISH 428

RESULT 4
AA472238
ID AAB72238 standard; protein; 428 AA.
XX
AC AAB72238;
XX 14-MAY-2001 (first entry)
DT Human CD39 like protein CD39-L4 amino acid sequence.
DE
XX Human CD39-like protein; apyrase; NDPase; platelet function inhibitor;
KW myocardial infarction; cerebral ischaemia; angina; arterial thrombosis;
KW cerebral artery thrombosis; platelet aggregation; inflammation;
KW apoptosis; autoimmune disorder; neurological disorder;
KW Alzheimer's disease; Parkinson's disease; cancer; CD39-L4.
XX

CC prophylaxis or treatment of inflammation related disorders, such as
 CC disorders involving sepsis or systemic inflammatory response syndrome or
 CC SIRS (and associated conditions such as fever, tachycardia, tachypnea,
 CC cytokine overstimulation); autoimmune disorders such as thrombosis,
 CC atherosclerosis, acute pancreatitis, dermatitis, including psoriasis,
 CC cirrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis;
 CC neurological disorders including neurodegenerative diseases, epilepsy,
 CC depression, Alzheimer's disease, Parkinson's disease, Huntington's
 CC disease, and amyotrophic lateral sclerosis; and cancer. The present
 CC sequence represents the CD39 like protein CD39-L4 amino acid sequence
 XX
 SQ Sequence 428 AA;

Query Match 99.2%; Score 2235; DB 4; Length 428;
 Best Local Similarity 99.3%; Pred. No. 4e-207;
 Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MATSGTFFMLVSVCSAVSHRNQOTWFEGLFLSSMCPINVSASTLYGIMFDAGSTGT 60
 Dd 1 MATSGTFFMLVSVCSAVSHRNQOTWFEGLFLSSMCPINVSASTLYGIMFDAGSTGT 60

Qy 61 RIHVYTFVQKMPGQLPILGEVDSVKPGLSAFVDPKQGAETVQGLLEVAKDSIPRSHW 120
 Dd 61 RIHVYTFVQKMPGQLPILGEVDSVKPGLSAFVDPKQGAETVQGLLEVAKDSIPRSHW 120

Qy 121 KKTPTVVLKATAGRLRLPEHKAKALLFEVKEIPFKSPFLVPKGSVSIIMTQDEGIPAWVTV 130
 Dd 121 KKTPTVVLKATAGRLRLPEHKAKALLFEVKEIPFKSPFLVPKGSVSIIMTQDEGIPAWVTV 130

Qy 181 NPLTQGLHGHROETVGTLDLGASTQITFLPOFKTLEQTPRGYLTSPFEMFNSTYKLYTH 240
 Dd 181 NPLTQGLHGHROETVGTLDLGASTQITFLPOFKTLEQTPRGYLTSPFEMFNSTYKLYTH 240

Qy 241 SYLGFGLKAARLALGALTEGTGHTFRSACLPRWLAEMIFPGVKYQYQGNQGEVGF 300
 Dd 241 SYLGFGLKAARLALGALTEGTGHTFRSACLPRWLAEMIFPGVKYQYQGNQGEVGF 300

Qy 301 EPCYAEVLVRVGRKLPQEEVORGSFYAFSYVYDRAVDTDMDYKGGILKVEDFERKAR 360
 Dd 301 EPCYAEVLVRVGRKLPQEEVORGSFYAFSYVYDRAVDTDMDYKGGILKVEDFERKAR 360

Qy 361 EVCNDLENFTSGSPFLCDLSYITALLKDGFGFADSTVLQTKKYNNTETQWALGATPHL 420
 Dd 361 EVCNDLENFTSGSPFLCDLSYITALLKDGFGFADSTVLQTKKYNNTETQWALGATPHL 420

Qy 421 LQSLGISH 428
 Dd 421 LQSLGISH 428

RESULT 6
 AAE19883
 ID AAE19883 standard; protein; 428 AA.

AC AAE19883;

DT 18-JUN-2002 (first entry)

DE Human CD39L4 protein.

XX Human; CD-39-like protein; CD39L4 protein; therapy; immune deficiency;
 KW autoimmune disorder; multiple sclerosis; systemic lupus erythematosus;
 KW rheumatoid arthritis; autoimmune thyroiditis; allergic reaction; asthma;
 KW insulin dependent diabetes mellitus; periodontal disease; osteoporosis;
 KW osteoarthritis; wound healing; tissue repair; Alzheimer's disease; ulcer;
 KW Parkinson's disease; amyotrophic lateral sclerosis; Huntington's disease;
 KW nervous system disease; nerve injury; ischaemia-reperfusion injury;
 KW endotoxin lethality; arthritis; nephritis; inflammatory bowel disease;
 KW Crohn's disease; virucide; antibacterial; antifungal; neuroprotective;
 KW dermatological; immunosuppressive; vulnary; neurotic; anticonvulsant;
 KW antiinflammatory; nephrotropic; gastrointestinal; vasotropic.

OS Homo sapiens.

XX US6350447-B1.
 PN
 XX 26-FEB-2002.
 PD
 XX 29-JAN-1999; 99US-00240639.
 PF
 XX 29-JAN-1999; 99US-00240639.
 PR
 XX (HYSE-) HYSEQ INC.
 PA
 XX Chadwick BP, Frischauf A;
 PI
 XX WPI; 2002-215262/27.
 DR
 XX N-PSDB; AAD31695.
 DR
 XX
 PT An isolated polypeptide with phosphohydrolase activity, designated
 PT CD39L2, useful to identify other proteins with which binding occurs or
 PT identify inhibitors and for treatment of, e.g., Alzheimer's, multiple
 PT sclerosis and osteoporosis.
 XX
 PS Example; Fig 7; 101pp; English.

The present invention relates to novel proteins with phosphohydrolase activity, designated CD-39-like (CD39L) proteins and polynucleotides encoding such proteins. CD39L proteins are useful to treat infectious diseases caused by viral, bacterial, fungal or other infection that may be treatable with CD39L. They are useful in the treatment of various immune deficiencies and disorders, autoimmune disorders such as multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune thyroiditis and insulin dependent diabetes mellitus, allergic reactions and conditions such as asthma and other respiratory problems, periodontal disease, osteoporosis, osteoarthritis and other tooth repair processes. They may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration as well as for wound healing and tissue repair and replacement and in the treatment of burns, incisions and ulcers. CD39L proteins may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central nervous system diseases such as Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, Huntington's disease, peripheral nervous system diseases peripheral nerve injuries, peripheral neuropathy and localised neuropathies. They are also used to treat mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. CD39L proteins of the invention are also useful to promote better or faster closure of non-healing wounds, including pressure ulcers, ulcers associated with vascular insufficiency and surgical and traumatic wounds. They also exhibit anti-inflammatory activity and may be used to treat inflammatory conditions including chronic or acute conditions), including ischaemia-reperfusion injury, endotoxin lethality, arthritis, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease or Crohn's disease. The present sequence is human CD39L4 protein

XX SQ Sequence 428 AA;

Query Match 99.2%; Score 2235; DB 5; Length 428;

Best Local Similarity 99.3%; Pred. No. 4e-207;

Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MATSGTFFMLVSVCSAVSHRNQOTWFEGLFLSSMCPINVSASTLYGIMFDAGSTGT 60
 Dd 1 MATSGTFFMLVSVCSAVSHRNQOTWFEGLFLSSMCPINVSASTLYGIMFDAGSTGT 60

Qy 61 RIHVYTFVQKMPGQLPILGEVDSVKPGLSAFVDPKQGAETVQGLLEVAKDSIPRSHW 120
 Dd 61 RIHVYTFVQKMPGQLPILGEVDSVKPGLSAFVDPKQGAETVQGLLEVAKDSIPRSHW 120

Qy 121 KKTPTVVLKATAGRLRLPEHKAKALLFEVKEIPFKSPFLVPKGSVSIIMTQDEGIPAWVTV 180
 Dd 121 KKTPTVVLKATAGRLRLPEHKAKALLFEVKEIPFKSPFLVPKGSVSIIMTQDEGIPAWVTV 180

Qy 181 NPLTQGLHGHROETVGTLDLGASTQITFLPOFKTLEQTPRGYLTSPFEMFNSTYKLYTH 240
 Dd 181 NPLTQGLHGHROETVGTLDLGASTQITFLPOFKTLEQTPRGYLTSPFEMFNSTYKLYTH 240

DB 181 NLTGQLHGRQETVGTLDLGASTQITFLPQFEKTLBQTPRGYLTSFEMFNSTYKLYTH 240
 QY 241 SYLGFLKAARLALCALTEGTDGHTFRSACLPRMLEAEHIFGQVKYQYGNQGEVGF 300
 DB 241 SYLGFLKAARLALCALTEGTDGHTFRSACLPRMLEAEHIFGQVKYQYGNQGEVGF 300
 QY 301 EPCVAEVLVRVGRKQHQPVEVQSGFYAFSYIYDRAVDTMDIDYKGGILKVEDFERKAR 360
 DB 301 EPCVAEVLVRVGRKQHQPVEVQSGFYAFSYIYDRAVDTMDIDYKGGILKVEDFERKAR 360
 QY 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQTKKNNIETGWLGCATPHL 420
 DB 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQTKKNNIETGWLGCATPHL 420
 QY 421 LOSLGISH 428
 DB 421 LOSLGISH 428

RESULT 7

AA444851

ID AAY44851 standard; protein; 405 AA.

AC AAY44851;

XX 18-MAY-2000 (first entry)

DT Human CD39-L66 protein.

DE Human CD39-L66 protein.

XX CD39-L66; human; CD39-L66; apyrase; nucleotide diphosphatase; NDPase;

XX ATP diphosphohydrolase; ATPase; adenosine diphosphate; ADP; treatment;

XX platelet aggregation; antithrombotic; thrombosis; myocardial infarction;

KW cerebral ischaemia; angina; vascular graft; extracorporeal circulation;

KW molecular weight marker; nutritional supplement; tumour; prevention;

KW drug targeting; splice variant.

XX Homo sapiens.

OS WO200004041-A2.

XX 27-JAN-2000.

XX 16-JUL-1999; 99WO-US016180.

XX 16-JUL-1998; 98US-00118205.

XX 24-JUL-1998; 98US-00122449.

XX 04-FEB-1999; 98US-00244444.

XX 19-MAR-1999; 98US-00273447.

XX 09-JUL-1999; 98US-00350836.

XX (HYSE-) HYSEQ INC.

XX Ford J, Mulero J;

XX WPI: 2000-182397/16.

XX N-PSDB; AA250358.

XX New nucleic acid encoding human CD39-like protein, useful for treating

XX and preventing thrombotic disease.

XX Claim 15; Page 124-125; 125pp; English.

XX The present amino acid sequence is the CD39-L66 protein, a splice variant

XX of the CD39-L66 protein. It is an apyrase and/or nucleotide diphosphatase

XX (NDPase), isolated from the human foetal liver-spleen cDNA library,

XX b2HPSIS20W. It is a soluble ATP diphosphohydrolase (ATPDase) and is

XX involved in the hydrolysis of adenosine diphosphate (ADP), the agonist

XX that causes platelet aggregation. CD39-L66 protein has 30% and 80%

XX homology to human and murine CD39. It has platelet aggregation inhibition

XX and antithrombotic activity. CD39-L66 is used to treat or prevent

XX thrombosis, myocardial infarction, cerebral ischaemia and angina. It is

XX also used in vitro, to maintain vascular grafts or during extracorporeal

XX circulation, to hydrolyse NDP, as molecular weight markers and as

CC nutritional supplements. It is used to identify therapeutic agents that
 CC bind and modulate CD39-L66. It is coupled to toxins for targeting drugs to
 CC tumours or other cells that express CD39-L66
 XX
 SQ Sequence 405 AA;

Query Match 92.8%; Score 2089; DB 3; Length 405;
 Best Local Similarity 99.2%; Pred. No. 4.9e-193;
 Matches 397; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MATSWGTVFPMVLVSCVSAVSHRNQOTWFEIGIFLSMCPINVSASTLYGIMFDAGSTGT 60
 DB 1 MATSWGTVFPMVLVSCVSAVSHRNQOTWFEIGIFLSMCPINVSASTLYGIMFDAGSTGT 60
 QY 61 RIHYTVFQVQMPQLPILEGVFDVSKPGLSAFVDPQKQAEVQGLLEVAKDSIPRSHW 120
 DB 61 RIHYTVFQVQMPQLPILEGVFDVSKPGLSAFVDPQKQAEVQGLLEVAKDSIPRSHW 120
 QY 121 KKTPTVLKATAGLRLLPEHKAKALLPEVKIIFRKSPLVPKGSVIMTGDGEGFAVTV 180
 DB 121 KKTPTVLKATAGLRLLPEHKAKALLPEVKIIFRKSPLVPKGSVIMTGDGEGFAVTV 180
 QY 181 NLTGQLHGRQETVGTLDLGASTQITFLPQFEKTLBQTPRGYLTSFEMFNSTYKLYTH 240
 DB 181 NLTGQLHGRQETVGTLDLGASTQITFLPQFEKTLBQTPRGYLTSFEMFNSTYKLYTH 240
 QY 241 SYLGFLKAARLALCALTEGTDGHTFRSACLPRMLEAEHIFGQVKYQYGNQGEVGF 300
 DB 241 SYLGFLKAARLALCALTEGTDGHTFRSACLPRMLEAEHIFGQVKYQYGNQGEVGF 300
 QY 301 EPCVAEVLVRVGRKQHQPVEVQSGFYAFSYIYDRAVDTMDIDYKGGILKVEDFERKAR 360
 DB 301 EPCVAEVLVRVGRKQHQPVEVQSGFYAFSYIYDRAVDTMDIDYKGGILKVEDFERKAR 360
 QY 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQ 400
 DB 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQ 400

RESULT 8

AA472239

ID AAB72239 standard; protein; 405 AA.

XX AAB72239;

XX 14-MAY-2001 (first entry)

XX Human CD39 like protein CD39-L66 amino acid sequence.

XX Human CD39-like protein; apyrase; NDPase; platelet function inhibitor;

XX myocardial infarction; cerebral ischaemia; angina; arterial thrombosis;

XX cerebral artery thrombosis; platelet aggregation; inflammation;

XX apoptosis; autoimmune disorder; neurological disorder;

XX Alzheimer's disease; Parkinson's disease; cancer; CD39-L66.

XX Homo sapiens.

XX WO200110205-A1.

XX 15-FEB-2001.

XX 09-AUG-2000; 2000WO-US021790.

XX 09-AUG-1999; 99US-00370265.

XX 11-JAN-2000; 2000US-00481238.

XX 25-APR-2000; 2000US-00557800.

XX 26-MAY-2000; 2000US-00583231.

XX 30-JUN-2000; 2000US-00608285.

XX (HYSE-) HYSEQ INC.

XX Ford J, Mulero JJ, Yeung G;

XX

DR WPI; 2001-147489/15.
DR N-PSDB; AAP63384.
XX
PT Polynucleotides encoding human CD39-like polypeptides, with apyrase
PT and/or NTPase activity, which are useful in the treatment of pathological
PT conditions caused by thrombosis (e.g. myocardial infarction) and
PT inflammatory disorders.
XX
PS Claim 17; Page 157-158; 203pp; English.
XX
CC This invention relates to polynucleotides encoding human CD39-like
CC polypeptides with apyrase and/or NTPase activity. The polypeptides having
CC ATPase, including NTPase, activity are useful for inhibiting platelet
CC function and can therefore be used in the prophylaxis or treatment of
CC pathological conditions caused by or involving thrombosis or excessive
CC coagulation or excessive platelet aggregation, such as myocardial
CC infarction, cerebral ischaemia, angina, arterial thrombosis, cerebral
CC artery thrombosis or intracardiac thrombosis, and conditions associated
CC with venous thrombosis. CD39-L4 and CD39-L2 polypeptides are useful in
CC modulating disease states (including platelet aggregation, inflammation
CC and apoptosis) associated with ADP or other purinergic signalling by
CC reducing the levels of NTPs. The polypeptides are also useful for
CC prophylaxis or treatment of inflammation related disorders, such as
CC disorders involving sepsis or systemic inflammatory response syndrome or
CC SIRS (and associated conditions such as fever, tachycardia, tachypnea,
CC cytokine overstimulation); autoimmune disorders such as thrombosis,
CC atherosclerosis, acute pancreatitis, dermatitis including psoriasis,
CC cirrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis,
CC neurological disorders including neurodegenerative diseases, epilepsy,
CC depression, Alzheimer's disease, Parkinson's disease, Huntington's
CC disease, and amyotrophic lateral sclerosis; and cancer. The present
CC sequence represents human CD39 like protein CD39-L4
XX
XX Sequence 405 AA;

Query Match 92.8%; Score 2089; DB 4; Length 405;
Best Local Similarity 99.2%; Pred. No. 4.9e-193;
Matches 397; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 MATSWGTVPFVFLVSCVSAVSHRNQOTWFGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSWGTVPFVFLVSCVSAVSHRNQOTWFGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
QY 61 RIHVYTFVQMPQQLPILGEVDSVKPKGLSAFVDQPKQASTVQGLLEVAKDSIPRSHW 120
DB 61 RIHVYTFVQMPQQLPILGEVDSVKPKGLSAFVDQPKQASTVQGLLEVAKDSIPRSHW 120
QY 121 KKTPTVTKATAGLRLLPEHKAKALLPEVKELPKKSPLVPKGSVSIWTCQDCIFAWVTV 180
DB 121 KKTPTVTKATAGLRLLPEHKAKALLPEVKELPKKSPLVPKGSVSIWTCQDCIFAWVTV 180
QY 181 NFLTGLQHGRQBTGTGLDGGASTQTITLPQFEKLTQTPRGYLTSPFEMFNSTYKLYTH 240
DB 181 NFLTGLQHGRQBTGTGLDGGASTQTITLPQFEKLTQTPRGYLTSPFEMFNSTYKLYTH 240
QY 241 SYLGFGLKAARLATLGALETGDTGHTFRSACLPRWLEAEWFGGVKYQYQGNQGEVGF 300
DB 241 SYLGFGLKAARLATLGALETGDTGHTFRSACLPRWLEAEWFGGVKYQYQGNQGEVGF 300
QY 301 EPCYAEVLVRVGRKLHQPEEVQSGSFYAFSYYYDRAVDTDMDIDYKGGILKVEDFERKAR 360
DB 301 EPCYAEVLVRVGRKLHQPEEVQSGSFYAFSYYYDRAVDTDMDIDYKGGILKVEDFERKAR 360
QY 361 EVCNDNLNFTSGSPFLCMDSLYITALLKDGFGFADSTVLQ 400
DB 361 EVCNDNLNFTSGSPFLCMDSLYITALLKDGFGFADSTVLQ 400

RESULT 9
AAE19884
ID AAE19884 standard; protein; 465 AA.
XX
AC AAE19884;

XX 18-JUN-2002 (first entry)
XX Mouse CD39L4 protein.
XX
XX Mouse; CD-39-like protein; CD39L4 protein; therapy; immune deficiency;
XX autoimmune disorder; multiple sclerosis; systemic lupus erythematosus;
XX rheumatoid arthritis; autoimmune thyroiditis; allergic reaction; asthma;
XX insulin dependent diabetes mellitus; periodontal disease; osteoporosis;
XX osteoarthritis; wound healing; tissue repair; Alzheimer's disease; ulcer;
XX Parkinson's disease; amyotrophic lateral sclerosis; Huntington's disease;
XX nervous system disease; nerve injury; ischaemia-reperfusion injury;
XX endotoxin lethality; arthritis; nephritis; inflammatory bowel disease;
XX Crohn's disease; virucide; antibacterial; antifungal; neuroprotective;
XX dermatological; immunosuppressive; vulnerary; nootropic; anticonvulsant;
XX antiinflammatory; nephrotropic; gastrointestinal; vasotropic; NTPase;
XX nucleotide-triphosphatase; enzyme.
XX
XX Mus musculus.
XX
XX US6350447-B1.
XX
XX 26-FEB-2002.
XX
XX 29-JAN-1999; 99US-00240639.
XX
XX 29-JAN-1999; 99US-00240639.
XX (HYSE-) HYSEQ INC.
XX
XX Chadwick BP, Frischauf A;
XX
XX WPI; 2002-215262/27.
XX
XX N-PSDB; AAD31696.
XX
XX An isolated polypeptide with phosphohydrolase activity, designated
XX CD39L2, useful to identify other proteins with which binding occurs or
XX identify inhibitors and for treatment of, e.g., Alzheimer's, multiple
XX sclerosis and osteoporosis.
XX
XX Example; Fig 1; 101pp; English.
XX
XX The present invention relates to novel proteins with phosphohydrolase
XX activity, designated CD-39-like (CD39L) proteins and polynucleotides
XX encoding such proteins. CD39L proteins are useful to treat infectious
XX diseases caused by viral, bacterial, fungal or other infection that may
XX be treatable with CD39L. They are useful in the treatment of various
XX immune deficiencies and disorders, autoimmune disorders such as multiple
XX sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune
XX thyroiditis and insulin dependent diabetes mellitus, allergic reactions
XX and conditions such as asthma and other respiratory problems, periodontal
XX disease, osteoporosis, osteoarthritis and other tooth repair processes.
XX They may have utility in compositions used for bone, cartilage, tendon,
XX ligament and/or nerve tissue growth or regeneration as well as for wound
XX healing and tissue repair and replacement and in the treatment of burns,
XX incisions and ulcers. CD39L proteins may also be useful for proliferation
XX of neural cells and for regeneration of nerve and brain tissue, i.e. for
XX the treatment of central nervous system diseases such as Alzheimer's
XX disease, Parkinson's disease, amyotrophic lateral sclerosis, Huntington's
XX disease, peripheral nervous system diseases peripheral nerve injuries,
XX peripheral neuropathy and localised neuropathies. They are also used to
XX treat mechanical and traumatic disorders which involve degeneration,
XX death or trauma to neural cells or nerve tissue. CD39L proteins of the
XX invention are also useful to promote better or faster closure of non-
XX healing wounds, including pressure ulcers, ulcers associated with
XX vascular insufficiency and surgical and traumatic wounds. They also
XX exhibit anti-inflammatory activity and may be used to treat inflammatory
XX conditions including chronic or acute conditions), including ischaemia-
XX reperfusion injury, endotoxin lethality, arthritis, nephritis, cytokine
XX or chemokine-induced lung injury, inflammatory bowel disease or Crohn's
XX disease. The present sequence is mouse CD39L4 protein, also known as
XX nucleotide-triphosphatase (NTPase)

SQ Sequence 465 AA;

Query Match 80.7%; Score 1817.5; DB 5; Length 465;
 Best Local Similarity 83.1%; Pred. No. 1.1e-166;
 Matches 349; Conservative 25; Mismatches 43; Indels 3; Gaps 3;

Qy 1 MATSGTGVFFMLVSVCSAVSHRNQQTWPEGIFLSMCPINVSASTLYGIMFDAGSTGT 60
 Db 1 MATSGAV-FMLIACVGVSTVYREQQTWEGVFLSSKCPINVSAGTFYIMFDAGSTGA 59

Qy 61 RIHYTTFVQKPGQGLPILEGVFDVSVRGELSAFVDQPKQAGATVQGLLELVAKDSIPRSHW 120
 Db 60 RIHYTTFVQKTAGQLPFLGIFBDSVRGELSAFVDQPKQAGATVQGLLELVAKDSIPRSHW 119

Qy 121 KKTFWLWKATAGLRLPHKAKALLEVEKTEIFRSPKSPFLVPGSVSINTGDEGIFAWTV 180
 Db 120 ERTFWLWKATAGLRLPHKAKALLEVEKTEIFRSPKSPFLVPGSVSINTGDEGIFAWTV 179

Qy 181 NFLGQLHGRQETVGTLDLGASTQTITFLPQPEKTLQTPRGYLTSPFEMFNSTYKLYTH 240
 Db 180 NFLGQLHGRQETVGTLDLGASTQTITFLPQPEKTLQTPRGYLTSPFEMFNSTYKLYTH 239

Qy 241 SYLFGGLKAARLATIGALETGTGHTFRSACLPRLAEWIFGSKVYQVGNQEGVGFP 300
 Db 240 SYLFGGLKAARLATIGALETGTGHTFRSACLPRLAEWIFGSKVYQVGNQEGVGFP 299

Qy 301 EPCYAEVLVRVGRKLPQPEVQVGSFYAFSYYYDRAVDTDMDYERKGGILKVEDFERKAR 360
 Db 300 EPCYAEVLVRVGRKLPQPEVQVGSFYAFSYYYDRAVDTDMDYERKGGILKVEDFERKAR 359

Qy 361 EVCNLENFTSGSPFLCMLDLSYITALLKDGFGPADSTVQLTKKVNNIETCWALGATPHL 420
 Db 360 EVCNLENFTSGSPFLCMLDLSYITALLKDGFGPADSTVQLTKKVNNIETCWALGATPHL 417

RESULT 10
 AAE53336
 ID AAE53336 standard; protein; 330 AA.
 AC AAE53336;
 XX
 XX
 XX 09-MAR-2001 (first entry)
 XX
 XX Human colon cancer antigen protein sequence SEQ ID NO:876.
 XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW identification; cytostatic; cardioactive; neuroprotective; vulnary;
 KW immunomodulatory; muscular; gynaecological; gastrointestinal;
 KW nephrotropic; antinefactive; antibacterial; gene therapy; wound;
 KW neural disorder; immune system disorder; muscular disorder;
 KW reproductive disorder; gastrointestinal disorder; renal disorder;
 KW infectious disease; cardiovascular disorder.
 XX
 XX Homo sapiens.
 XX
 XX WO200055351-A1.
 XX
 XX 21-SEP-2000.
 XX
 XX 08-MAR-2000; 2000WO-US005883.
 XX
 XX 12-MAR-1999; 99US-0124270P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Ruben SM;
 XX
 XX WPI; 2000-587534/55.
 XX
 XX N-PSDB; AAC98093.
 XX
 XX Colon cancer associated gene sequences, referred to as colon cancer
 PT antigens, useful for the treatment, prevention, and diagnosis of colon
 PT disorders such as colon cancer.

XX Claim 11; Page 1429-1431; 2104pp; English.
 XX AAC97991 to AAC98763 encode the human colon cancer associated proteins,
 CC called human colon cancer antigens, given in AAE53234 to AAE54006. The
 CC human colon cancer antigens can have cytostatic, cardioactive, muscular;
 CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal, and
 CC vulnary, nephrotropic, antinefactive and antibacterial activities, and
 CC can be used in gene therapy. The colon cancer antigen polynucleotides,
 CC proteins and antibodies to the proteins are useful for the prevention,
 CC treatment and diagnosis of colon disorders, such as colon cancer. The
 CC polynucleotides may be used in diagnostics and research, such as for
 CC chromosome identification, and as hybridisation probes. The proteins may
 CC also be used to prevent diseases such as neural disorders, immune system
 CC disorders, muscular disorders, reproductive disorders, gastrointestinal
 CC disorders, wounds, renal disorders, infectious diseases, and
 CC cardiovascular disorders. AAC98764 to AAC98772 and AAE54007 represent
 CC sequences used in the exemplification of the present invention
 XX
 SQ Sequence 330 AA;
 Query Match 73.0%; Score 1645; DB 3; Length 330;
 Best Local Similarity 96.3%; Pred. No. 3.3e-150;
 Matches 316; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 101 AETVQGLLELVAKDSIPRSHWKTTPVVLKATAGLRLPHKAKALLEVEKTEIFRSPFLVP 160
 Db 3 ARAVQGLLELVAKDSIPRSHWKTTPVVLKATAGLRLPHKAKALLEVEKTEIFRSPFLVP 62

Qy 161 KGSVSIWTDGEGIFAWTVNFLTQGLHGRQETVGTLDLGASTQTITFLPQPEKTLQET 220
 Db 63 KGSVSIWTDGEGIFAWTVNFLTQGLHGRQETVGTLDLGASTQTITFLPQPEKTLQET 122

Qy 221 PRGYLTSPFEMFNSTYKLYTHSYLFGGLKAARLATIGALETGTGHTFRSACLPRLAE 280
 Db 123 PRGYLTSPFEMFNSTYKLYTHSYLFGGLKAARLATIGALETGTGHTFRSACLPRLAE 182

Qy 281 WIFGVKYQVGNQEGVGPEPCYAEVLVRVGRKLPQPEVQVGSFYAFSYYYDRAVDTD 340
 Db 183 WIFGVKYQVGNQEGVGPEPCYAEVLVRVGRKLPQPEVQVGSFYAFSYYYDRAVDTD 242

Qy 341 MIDYERKGGILKVEDFERKAREVCNLENFTSGSPFLCMLDLSYITALLKDGFGPADSTVQL 400
 Db 243 MIDYERKGGILKVEDFERKAREVCNLENFTSGSPFLCMLDLSYITALLKDGFGPADSTVQL 302

Qy 401 LTKKVNNIETCWALGATPHLQSLGISH 428
 Db 303 LTKKVNNIETCWALGATPHLQSLGISH 330

RESULT 11
 AAE19881
 ID AAE19881 standard; protein; 456 AA.
 AC AAE19881;
 XX
 XX 18-JUN-2002 (first entry)
 XX
 XX Human CD39L2 protein.
 XX Human; CD-39-like protein; CD39L2 protein; therapy; immune deficiency;
 KW autoimmune disorder; multiple sclerosis; systemic lupus erythematosus;
 KW rheumatoid arthritis; autoimmune thyroiditis; allergic reaction; asthma;
 KW insulin dependent diabetes mellitus; periodontal disease; osteoporosis;
 KW osteoarthritis; wound healing; tissue repair; Alzheimer's disease; ulcer;
 KW Parkinson's disease; amyotrophic lateral sclerosis; Huntington's disease;
 KW nervous system disease; nerve injury; ischaemia-reperfusion injury;
 KW endotoxin lethality; arthritis; nephritis; inflammatory bowel disease;
 KW Crohn's disease; virucide; antibacterial; antifungal; neuroprotective;
 KW dermatological; immunosuppressive; vulnary; nontropic; anticonvulsant;
 KW antiinflammatory; nephrotropic; gastrointestinal; vasotropic.
 XX
 XX Homo sapiens.
 OS

XX US6350447-B1.
 PN 26-FEB-2002.
 XX 29-JAN-1999; 99US-00240639.
 XX 29-JAN-1999; 99US-00240639.
 PF (HYSE-) HYSEQ INC.
 XX Chadwick BP, Frischauf A;
 XX WPI; 2002-215262/27.
 DR N-PSDB; AAD31693.
 XX An isolated polypeptide with phosphohydrolase activity, designated
 PT CD39L2, useful to identify other proteins with which binding occurs or
 PT identify inhibitors and for treatment of, e.g., Alzheimer's, multiple
 PT sclerosis and osteoporosis.
 XX Claim 1; Fig 4; 101pp; English.
 PS The present invention relates to novel proteins with phosphohydrolase
 CC activity, designated CD-39-like (CD39L) proteins and polynucleotides
 CC encoding such proteins. CD39L proteins are useful to treat infectious
 CC diseases caused by viral, bacterial, fungal or other infection that may
 CC be treatable with CD39L. They are useful in the treatment of various
 CC immune deficiencies and disorders, autoimmune diseases such as multiple
 CC sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune
 CC thyroiditis and insulin dependent diabetes mellitus, allergic reactions
 CC and conditions such as asthma and other respiratory problems, periodontal
 CC disease, osteoporosis, osteoarthritis and other tooth repair processes.
 CC They may have utility in compositions used for bone, cartilage, tendon,
 CC ligament and/or nerve tissue growth or regeneration as well as for wound
 CC healing and tissue repair and replacement and in the treatment of burns,
 CC incisions and ulcers. CD39L proteins may also be useful for proliferation
 CC of neural cells and for regeneration of nerve and brain tissue, i.e. for
 CC the treatment of central nervous system diseases such as Alzheimer's
 CC disease, Parkinson's disease, amyotrophic lateral sclerosis, Huntington's
 CC disease, peripheral nervous system diseases peripheral nerve injuries,
 CC peripheral neuropathy and localised neuropathies. They are also used to
 CC treat mechanical and traumatic disorders which involve degeneration,
 CC death or trauma to neural cells or nerve tissue. CD39L proteins of the
 CC invention are also useful to promote better or faster closure of non-
 CC healing wounds including pressure ulcers, ulcers associated with
 CC vascular insufficiency and surgical and traumatic wounds. They also
 CC exhibit anti-inflammatory activity and may be used to treat inflammatory
 CC conditions including chronic or acute conditions, including ischaemia-
 CC reperfusion injury, endotoxin lethality, arthritis, nephritis, cytokine
 CC or chemokine-induced lung injury, inflammatory bowel disease or Crohn's
 CC disease. The present sequence is human CD39L2 protein
 XX Sequence 456 AA;
 SQ Query Match 44.2%; Score 996; DB 5; Length 456;
 Best Local Similarity 52.4%; Pred. No. 3.5e-87;
 Matches 204; Conservative 54; Mismatches 125; Indels 6; Gaps 4;
 QY 40 PINVSA---STLVGIMFDAGSTGRHIVYTVQKPCQLPLLEGVPSVKPGLSAFVDQ 96
 DB 62 PLGTAAAGHGVYGYIMFDAGSTGRHIVYTVQKPCQLPLLEGVPSVKPGLSAFVDQ 120
 QY 97 PKQAGTAVQGLLEKADSIKPSHWKKTFFVLXATAGLRLPEKAKALLFEVKEIRKSP 156
 DB 121 VEKSAQGIKRELLDVAQDIPDFWKATPLVLKATAGLRLPEKAKALLFEVKEIRKSP 180
 QY 157 FLVPKGSVSMGQDEGIPAWTVNPLTQGLHGRQETVGTLDGGASTQITLPOPEKT 216
 DB 181 FLVGDDCVSNMGDEGVSAWITNFLTGSLTKPGSSGVKLDLGGSGTQIAFLPRVEGT 240
 QY 217 LEQTPRGVLTYSFENFNSYKLYTHSYLGFGLKARLATLGALETG-ETDGTFRSACLPR 275

DB 241 LOASPPGVLTAIRNFNTYKLYSYLGLGMSARLAILGGVEQPAKDGKELVSPCLSP 300
 QY 276 WLEAEWIFGGYKYQVGNQGEVGFPCYAEVLVRVVRKGLHQPBEVQSGSFYAFSYYYDR 335
 DB 301 SFKGEWEHAEVTYRVSGOKAAASLHELCAARVSEVLQNRVHRTBEVKHVDYAFSYYYDL 360
 QY 336 AVDTMDIDYEGGILKVEDPERKAREVCDNLENFTSGSPFLQMDLSYITALLKDGFGFAD 395
 DB 361 AAGVGLIDAEKGGSLVGDPEIAKYVCTIETOPQSFSSCKDLTYVSLLLQE-FGFPR 419
 QY 396 STVLQLTKKVNNIETGVALGATPHLLQSL 424
 DB 420 SKVLKLRKIDNVETSWALGAIFHVIDSL 448
 RESULT 12
 AAB72241
 ID AAB72241 standard; protein; 484 AA.
 XX AAB72241;
 AC AAB72241;
 XX 14-MAY-2001 (first entry)
 DT Human CD39 like protein CD39-L2 amino acid sequence.
 DE Human CD39-like protein, apyrase; NDPase; platelet function inhibitor;
 KW myocardial infarction; cerebral ischaemia; angina; arterial thrombosis;
 KW cerebral artery thrombosis; platelet aggregation; inflammation;
 KW apoptosis; autoimmune disorder; neurological disorder;
 KW Alzheimer's disease; Parkinson's disease; cancer; CD39-L2.
 OS Homo sapiens.
 XX WO200110205-A1.
 PN 15-FEB-2001.
 PD 09-AUG-2000; 2000MO-US021790.
 XX 09-AUG-1999; 99US-00370265.
 PR 11-JAN-2000; 2000US-00481238.
 PR 25-APR-2000; 2000US-00557800.
 PR 26-MAY-2000; 2000US-00583231.
 PR 30-JUN-2000; 2000US-00608285.
 XX (HYSE-) HYSEQ INC.
 XX Ford J, Mulero JJ, Yeung G;
 PI WPI; 2001-147489/15.
 XX N-PSDB; AAF63386.
 DR Polynucleotides encoding human CD39-like polypeptides, with apyrase
 PT and/or NDPase activity, which are useful in the treatment of pathological
 PT conditions caused by thrombosis (e.g. myocardial infarction) and
 PT inflammatory disorders.
 XX Claim 39; Page 162-164; 203pp; English.
 PS This invention relates to polynucleotides encoding human CD39-like
 CC polypeptides with apyrase and/or NDPase activity. The polypeptides having
 CC ATPase, including NDPase, activity are useful for inhibiting platelet
 CC function and can therefore be used in the prophylaxis or treatment of
 CC pathological conditions caused by or involving thrombosis or excessive
 CC coagulation or excessive platelet aggregation, such as myocardial
 CC infarction, cerebral ischaemia, angina, arterial thrombosis, cerebral
 CC artery thrombosis or intracardiac thrombosis, and conditions associated
 CC with venous thrombosis. CD39-L4 and CD39-L2 polypeptides are useful in
 CC modulating disease states (including platelet aggregation, inflammation
 CC and apoptosis) associated with ADP or other purinergic signalling by
 CC reducing the levels of NDPs. The polypeptides are also useful for
 CC prophylaxis or treatment of inflammation related disorders, such as
 CC disorders involving sepsis or systemic inflammatory response syndrome or

Db 427 SKVLKTRKIDNVETSWALGAFHYIDSL 455

RESULT 14

ABJ04657 standard; protein; 467 AA.

AC ABJ04657;

DT 11-OCT-2002 (first entry)

DE Protein of NOVX 15a SEQ ID No 36.

CC Cytostatic; antidiabetic; anorectic; metabolic; nootropic; antilipaeamic;
 CC neuroprotective; antiparkinsonian; anticonvulsant; cerebroprotective;
 CC tranquiliser; neuroleptic; antidiabetic; antitumor; antiinflammatory;
 CC anti-HIV; antiallergic; antirheumatic; antiarthritic; NOVX; diabetes;
 CC metabolic disorder; obesity; infectious disease; Alzheimer's disease;
 CC anorexia; neurodegenerative disorder; Parkinson's disorder; obesity;
 CC immune disorder; haematopoietic disorder; dyslipidaemia; chronic disease;
 CC metabolic syndrome X; wasting disorder; cancer; neurological disorder;
 CC epilepsy; stroke; mental disorder; schizophrenic disorders; goiter;
 CC vesicular transport; cystic fibrosis; gastrointestinal disorder;
 CC diabetes mellitus; ulcerative colitis; AIDS; allergic reaction;
 CC multiple sclerosis; rheumatoid arthritis; transgenic animal;
 CC gene therapy.

XX Unidentified.

OS W0200246409-A2.

XX 13-JUN-2002.

XX 06-DEC-2001; 2001NO-US046586.

XX 06-DEC-2000; 2000US-0251560P.

XX 12-DEC-2000; 2000US-0255029P.

XX 08-JAN-2001; 2001US-0260326P.

XX 24-JAN-2001; 2001US-0263800P.

XX 20-FEB-2001; 2001US-0269942P.

XX 24-APR-2001; 2001US-0286183P.

XX 20-AUG-2001; 2001US-0313627P.

XX 12-SEP-2001; 2001US-0318712P.

XX (CURA-) CURAGEN CORP.

XX Guo X, Li L, Patturajan M, Shimkets RA, Casman SJ, Malyankar UM;

XX Tchernev VT, Vernet CAM, Spytek KA, Shenoy SG, Aisobrook JP;

XX Edinger S, Peyman JA, Stone DJ, Ellerman K, Gangolli EA, Boldog FL;

XX Colman SD, Eisen AJ, Liu X, Padigaru M, Spaderna SK, Zerhusen BD;

XX WPI: 2002-547774/58.

XX N-PSDB; ABT05470.

XX Novel isolated polypeptide, designated NOVX, useful for treating or

XX preventing cancer, diabetes, obesity, dyslipidemia, anorexia, and

XX metabolic, neurodegenerative, immune and hematopoietic disorders.

XX Claim 1; Page 140; 421pp; English.

XX The invention relates to an isolated polypeptide, designated NOVX,

XX comprising a sequence fully defined in the specification. The isolated

XX protein, its encoding polynucleotide or an antibody created from the

XX protein is useful in the manufacture of a medicament for treating a

XX syndrome associated with a human disease, preferably a NOVX-associated

CC chronic diseases, and cancer. The isolated protein, its encoding
 CC polynucleotide or an antibody created from the protein are useful for
 CC treating or preventing neurological disorders such as epilepsy, stroke,
 CC mental disorders including mood, anxiety, schizophrenic disorders,
 CC disorders of vesicular transport such as cystic fibrosis, diabetes
 CC mellitus, goiter, gastrointestinal disorders including ulcerative
 CC colitis, other conditions associated with abnormal vesicle trafficking
 CC including AIDS, allergic reactions, multiple sclerosis and rheumatoid
 CC arthritis. A cell comprising the vector of the invention is useful for
 CC producing non-human transgenic animals. The polynucleotide of the
 CC invention can be used to treat disorders by gene therapy. This sequence
 CC represents one of the isolated NOVX proteins of the invention
 XX

XX Sequence 467 AA;

Query Match 44.1%; Score 993; DB 5; Length 467;

Best Local Similarity 52.2%; Pred. No. 7e-87;

Matches 203; Conservative 55; Mismatches 125; Indels 6; Gaps 4;

QY 40 PINVSA---STLYGIMFDAGSTGTHIHYVTFQVMPCQLPILEGEVDSVKGLSAFYDQ 96

DB 73 PLGTAADGHEVYGYIMFDAGSTGTRVHVQFT-RPPRETPTLTHTFKALKEGLSAYADD 131

QY 97 PKQGAETVOGLLEVAKDSIPRSHMKKTIPWLKATAGLLEPEHAKALLFEVKEIFRKSP 156

DB 132 VEKSAQGIREDLDVAKQDIPYDFWKATPLVLKATAGLLEPEHAKALLFEVKEIFRKSP 191

QY 157 FLVPGKSVSIMTQDEGIFAWVTNPLTGLQHGHRQETVGLDGGASTQITFLPQFEXT 216

DB 192 FLVGGDCVSIIMNGTDEGVSAWITINFLTGLSLKTPGSSVGMIDLGSGSTQIAFLPRVREGT 251

QY 217 LEOTPRGYLTSEFMENSTYKLYTHSYLGFGKKAARLATLGALETE-GTDGHTFRSACLPR 275

DB 252 LQASPPGYLTALRMENRTYKLYSYLGGLMSARLAILGGVGGPAPKDKGLNSPCLSP 311

QY 276 WLEAEWIFGVKYQYGNQGEVGPPEPCYAEVLRVVRKGLHQPEVQSGSFVAPSYTYDR 335

DB 312 SPKEGEWAHEAVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTTEVSKHVDYFAPSYTYDL 371

QY 336 AVDTMDIDYKGGILLKVEDFERKAREVCNLENFTSGSPCLMDLSYITALLKDGFGPAD 395

DB 372 AAGVGLIDABKGSLVVGDFEFAAKYIVCTLETQPSQSPFFSCMDLTYVSLLLQE-FGPR 430

QY 396 STVLQLTKKVANNIETGNALGATFHLLOSL 424

DB 431 SKVLKTRKIDNVETSWALGAFHYIDSL 459

RESULT 15

AAM93929

ID AAM93929 standard; protein; 456 AA.

XX AAM93929;

XX 06-NOV-2001 (first entry)

XX Human polypeptide, SEQ ID NO: 4100.

XX Human; full length cDNA; cDNA synthesis; oligo-capping.

XX Homo sapiens.

XX EP1130094-A2.

XX 05-SEP-2001.

XX 07-JUL-2000; 2000EP-00114089.

XX 08-JUL-1999; 99JP-00194486.

XX 11-JAN-2000; 2000JP-00118774.

XX 02-MAY-2000; 2000JP-00183765.

XX (HELI-) HELIX RES INST.

Search completed: July 1, 2004, 13:46:37
Job time : 53 secs


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Db 121 KKTVPVVKATAGLRLPEHKAKALLFEVKELFRKSPFLVPKGSVIMDSGDEGLAWTV 180
Qy 181 NFLTQGLHGRQETVGTLDLGGASTQITFLPQPEKTLQTPRGYLTSEFNFNSTYKLYTH 240
Db 181 NFLTQGLHGRQETVGTLDLGGASTQITFLPQPEKTLQTPRGYLTSEFNFNSTYKLYTH 240
Qy 241 SYLGFGKKAARLATIAGLETGTGHTFRSACLPRWLEAEWIFGVKYQYGGNQBGEVGF 300
Db 241 SYLGFGKKAARLATIAGLETGTGHTFRSACLPRWLEAEWIFGVKYQYGGNQBGEVGF 300
Qy 301 EPCVAEVLVRVGRKGLHOPEEVRGSGFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
Db 301 EPCVAEVLVRVGRKGLHOPEEVRGSGFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
Qy 361 EVCNLENFTSGSPFLCMLDLSYITALLKDGFGFADSTVLQ 420
Db 361 EVCNLENFTSGSPFLCMLDLSYITALLKDGFGFADSTVLQ 420
Qy 421 LQSIGISH 428
Db 421 LQSIGISH 428

RESULT 2
Q8WUB3 PRELIMINARY; PRT; 407 AA.
AC Q8WUB3, 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Similar to eotonucleoside triphosphate diphosphohydrolase 5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RX STRAIN=C57BL/6J; TISSUE=Testis;
RA The PANTOM Consortium.
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AC031581; BAC27461.1; -.
DR MGD; AGI:1321385; Entpd5.
DR InterPro; IPR000407; GDAI_CD39_NTPase.
DR Pfam; PF01150; GDAI_CD39; 1.
SQ SEQUENCE 407 AA; 45336 MW; D92A5F7DC9EC9E5B CRC64;

Query Match 92.8%; Score 2089; DB 4; Length 407;
Best Local Similarity 99.2%; Pred. No. 1.8e-171; Indels 0; Gaps 0;
Matches 397; Conservative 0; Mismatches 3;

Qy 1 MATSWGTVFFMLVSVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
Db 1 MATSWGTVFFMLVSVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
Qy 61 RIHYTTFVQKMPGQPLILEGEVFDSPKGLSAFVDQPKQGAETVQGLLEAKDSIPRSHW 120
Db 61 RIHYTTFVQKMPGQPLILEGEVFDSPKGLSAFVDQPKQGAETVQGLLEAKDSIPRSHW 120
Qy 121 KKTVPVVKATAGLRLPEHKAKALLFEVKELFRKSPFLVPKGSVIMDSGDEGLAWTV 180
Db 121 KKTVPVVKATAGLRLPEHKAKALLFEVKELFRKSPFLVPKGSVIMDSGDEGLAWTV 180
Qy 181 NFLTQGLHGRQETVGTLDLGGASTQITFLPQPEKTLQTPRGYLTSEFNFNSTYKLYTH 240
Db 181 NFLTQGLHGRQETVGTLDLGGASTQITFLPQPEKTLQTPRGYLTSEFNFNSTYKLYTH 240
Qy 241 SYLGFGKKAARLATIAGLETGTGHTFRSACLPRWLEAEWIFGVKYQYGGNQBGEVGF 300
Db 241 SYLGFGKKAARLATIAGLETGTGHTFRSACLPRWLEAEWIFGVKYQYGGNQBGEVGF 300
Qy 301 EPCVAEVLVRVGRKGLHOPEEVRGSGFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
Db 301 EPCVAEVLVRVGRKGLHOPEEVRGSGFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
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Db 301 EPCVAEVLVRVGRKGLHOPEEVRGSGFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
Qy 361 EVCNLENFTSGSPFLCMLDLSYITALLKDGFGFADSTVLQ 400
Db 361 EVCNLENFTSGSPFLCMLDLSYITALLKDGFGFADSTVLQ 400

RESULT 3
Q8CD29 PRELIMINARY; PRT; 427 AA.
AC Q8CD29, 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 5.
GN ENTPD5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium.
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK031581; BAC27461.1; -.
DR MGD; AGI:1321385; Entpd5.
DR InterPro; IPR000407; GDAI_CD39_NTPase.
DR Pfam; PF01150; GDAI_CD39; 1.
SQ SEQUENCE 427 AA; 47101 MW; 6E3773C842B58477 CRC64;

Query Match 87.7%; Score 1975.5; DB 11; Length 427;
Best Local Similarity 87.4%; Pred. No. 1.2e-161; Indels 1; Gaps 1;
Matches 373; Conservative 25; Mismatches 28;

Qy 1 MATSWGTVFFMLVSVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
Db 1 MATSWGTVFFMLVSVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 59
Qy 61 RIHYTTFVQKMPGQPLILEGEVFDSPKGLSAFVDQPKQGAETVQGLLEAKDSIPRSHW 120
Db 61 RIHYTTFVQKMPGQPLILEGEVFDSPKGLSAFVDQPKQGAETVQGLLEAKDSIPRSHW 119
Qy 121 KKTVPVVKATAGLRLPEHKAKALLFEVKELFRKSPFLVPKGSVIMDSGDEGLAWTV 180
Db 121 KKTVPVVKATAGLRLPEHKAKALLFEVKELFRKSPFLVPKGSVIMDSGDEGLAWTV 179
Qy 181 NFLTQGLHGRQETVGTLDLGGASTQITFLPQPEKTLQTPRGYLTSEFNFNSTYKLYTH 240
Db 181 NFLTQGLHGRQETVGTLDLGGASTQITFLPQPEKTLQTPRGYLTSEFNFNSTYKLYTH 239
Qy 241 SYLGFGKKAARLATIAGLETGTGHTFRSACLPRWLEAEWIFGVKYQYGGNQBGEVGF 300
Db 241 SYLGFGKKAARLATIAGLETGTGHTFRSACLPRWLEAEWIFGVKYQYGGNQBGEVGF 299
Qy 301 EPCVAEVLVRVGRKGLHOPEEVRGSGFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
Db 301 EPCVAEVLVRVGRKGLHOPEEVRGSGFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 359
Qy 361 EVCNLENFTSGSPFLCMLDLSYITALLKDGFGFADSTVLQ 420
Db 361 EVCNLENFTSGSPFLCMLDLSYITALLKDGFGFADSTVLQ 419
Qy 421 LQSIGISH 427
Db 421 LQSIGISH 426
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function).

DE OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RA Strauberg R.;

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR ENBL; BC025980; AAH25980.1; -.

DR GO; GO:0016787; F:hydrolyase activity; IEA.

DR InterPro; IPR000407; GDA1_CD39_NTPase.

DR Pfam; PF01150; GDA1_CD39_1.

KN Hydrolase.

SQ SEQUENCE 483 AA; 53119 MW; A850E5035BCDC8F CRC64;

Query Match 44.1%; Score 993; DS 4; Length 483;

Best Local Similarity 52.2%; Pred. No. 7.7e-77;

Matches 203; Conservative 55; Mismatches 125; Indels 6; Gaps 4

Qy 40 PINVSA--STLYGIMFDAGSTGTHVYTPVQKMPGQLPILGEVFDVSKPGLSAFVDQ 96

Db 89 PLGTAADGHEVYFYGIMFDAGSTGTRVHVQFT-PPRETPTLTHTTFKALPKGUSAYADD 147

Qy 97 PKQGAETVQGLLEVAKDSIPRSHWKTTPVLKATAGLRLPEHKAALLFFVXBIFRKSP 156

Db 148 VEKSAGGIRELLDVAQDIPDPFWKATPLVLKATAGLRLPEKKAQKLQKXKVEFKASP 207

Qy 157 FLVPGKGSVIMTQDQEGIPAWVTNPLTQGLHGRQETVGTLDLGGASTQTTFIPQFRT 216

Db 208 FLVGGDCVINGTDEGVSAWITINPLTGLSLTPOGSSVGMGLDGGGSGTQIAFLPRVEGT 267

Qy 217 LEOTPRGYLTSEMFNSTVLYTHSYLGFGLKAARLATLGALETB-GTDGHTFRSACLPR 275

Db 268 LQASPGYLTALRMFNRYTKLSYSLGLGLMSARLATLGGVEGPAKDGKELVSPCLSP 327

Qy 276 WLBAEWIPGGVKYQYGGNQESEVGFPCVAVRVLVRGKLHOPVEVQSGSVAFSYYYDR 335

Db 328 SFKGEWEHAEVTVYSGQKAAASLHSLCAARVSEVLQNRVHRTVEVGVDFVAFSYYYDL 387

Qy 336 AVDTOMIDYKGGILKVEDFERKARVCDNLENFTSGSPFLCMDLSYITALLKDGPGFAD 395

Db 388 AGVGLIDAEKGGSLVVGDFEIAAKYVCTRLETPQSPFSCMDLTYVSLLLQK-FGPR 446

Qy 396 STVLOLTKVNNIETGALGFHLLQSL 424

Db 447 SXVLKLRKIDNVETSWALGAIFHYIDSL 475

RESULT 6

Q725B5 PRELIMINARY; PRT; 484 AA.

ID Q725B5

AC Q725B5; (TREMELrel. 25, Created)

DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

DE CD39L2 nucleotidase.

GN ENTPD6.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Ivanenkov V.V., Murphy-Piedmonte D.M., Kirley T.L.;

RT "Bacterial Expression, Characterization, and Disulfide Bond Determination of Soluble Human NTPDase6 (CD39L2) Nucleotidase: Implications for Structure and Function.";

RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

DR ENBL; AY327581; AAP92131.1; -.

SQ SEQUENCE 484 AA; 53274 MW; D00A5D2915DF36CE CRC64;

function).

DE OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Ivanenkov V.V., Murphy-Piedmonte D.M., Kirley T.L.;

RT "Bacterial Expression, Characterization, and Disulfide Bond Determination of Soluble Human NTPDase6 (CD39L2) Nucleotidase: Implications for Structure and Function.";

RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

DR ENBL; AY327581; AAP92131.1; -.

SQ SEQUENCE 484 AA; 53274 MW; D00A5D2915DF36CE CRC64;

function).

DE OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Ivanenkov V.V., Murphy-Piedmonte D.M., Kirley T.L.;

RT "Bacterial Expression, Characterization, and Disulfide Bond Determination of Soluble Human NTPDase6 (CD39L2) Nucleotidase: Implications for Structure and Function.";

RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

DR ENBL; AY327581; AAP92131.1; -.

SQ SEQUENCE 484 AA; 53274 MW; D00A5D2915DF36CE CRC64;

function).

DE OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Ivanenkov V.V., Murphy-Piedmonte D.M., Kirley T.L.;

RT "Bacterial Expression, Characterization, and Disulfide Bond Determination of Soluble Human NTPDase6 (CD39L2) Nucleotidase: Implications for Structure and Function.";

RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

DR ENBL; AY327581; AAP92131.1; -.

SQ SEQUENCE 484 AA; 53274 MW; D00A5D2915DF36CE CRC64;

function).

DE OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Ivanenkov V.V., Murphy-Piedmonte D.M., Kirley T.L.;

RT "Bacterial Expression, Characterization, and Disulfide Bond Determination of Soluble Human NTPDase6 (CD39L2) Nucleotidase: Implications for Structure and Function.";

RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

DR ENBL; AY327581; AAP92131.1; -.

SQ SEQUENCE 484 AA; 53274 MW; D00A5D2915DF36CE CRC64;

function).

DE OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Ivanenkov V.V., Murphy-Piedmonte D.M., Kirley T.L.;

RT "Bacterial Expression, Characterization, and Disulfide Bond Determination of Soluble Human NTPDase6 (CD39L2) Nucleotidase: Implications for Structure and Function.";

RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

DR ENBL; AY327581; AAP92131.1; -.

SQ SEQUENCE 484 AA; 53274 MW; D00A5D2915DF36CE CRC64;

function).

DE OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Ivanenkov V.V., Murphy-Piedmonte D.M., Kirley T.L.;

RT "Bacterial Expression, Characterization, and Disulfide Bond Determination of Soluble Human NTPDase6 (CD39L2) Nucleotidase: Implications for Structure and Function.";

RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

DR ENBL; AY327581; AAP92131.1; -.

SQ SEQUENCE 484 AA; 53274 MW; D00A5D2915DF36CE CRC64;

function).

DE OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Ivanenkov V.V., Murphy-Piedmonte D.M., Kirley T.L.;

RT "Bacterial Expression, Characterization, and Disulfide Bond Determination of Soluble Human NTPDase6 (CD39L2) Nucleotidase: Implications for Structure and Function.";

RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

DR ENBL; AY327581; AAP92131.1; -.

SQ SEQUENCE 484 AA; 53274 MW; D00A5D2915DF36CE CRC64;

function).

DE OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Ivanenkov V.V., Murphy-Piedmonte D.M., Kirley T.L.;

RT "Bacterial Expression, Characterization, and Disulfide Bond Determination of Soluble Human NTPDase6 (CD39L2) Nucleotidase: Implications for Structure and Function.";

RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

DR ENBL; AY327581; AAP92131.1; -.

SQ SEQUENCE 484 AA; 53274 MW; D00A5D2915DF36CE CRC64;

function).

DE OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Ivanenkov V.V., Murphy-Piedmonte D.M., Kirley T.L.;

RT "Bacterial Expression, Characterization, and Disulfide Bond Determination of Soluble Human NTPDase6 (CD39L2) Nucleotidase: Implications for Structure and Function.";

RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

DR ENBL; AY327581; AAP92131.1; -.

SQ SEQUENCE 484 AA; 53274 MW; D00A5D2915DF36CE CRC64;

function).

DE OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Cat


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Query Match 44.1%; Score 993; DB 4; Length 484;
Best Local Similarity 52.2%; Pred. No. 7.8e-77;
Matches 203; Conservative 55; Mismatches 125; Indels 6; Gaps 4;

QY 40 PINVSA---STLYGIMFDAGSTGTRIHYVTFVQKMPGQLPILGEVDFSVKPGLSAFVDQ 96
DB 90 PLGTAADGHEVYFGIMFDAGSTGTRVHVQFT-RPPRETPTLTHTFTKALPKGLSAYADD 148
QY 97 PQGAEITVQGLLEVAKDSIPRSHMKKTFWLKAATAGLRLPEHAKALLFEVKRSP 156
DB 149 VKSAQGIKRELLDVAKQDIPDFWKATPLVLKATAGLRLPEHAKALLQKVKVFRASP 208
QY 157 FLVPKGSVSIWQDEGIPFAMVTNVLFCQLHGRQETVGLDGGASTQITFLPQFEXT 216
DB 209 FLVGGDCVSIWNGTDEGVSAMITINFLTGSLSKTPGSSVGMGLDGGSTQIAFLPRVEGT 268
QY 217 LEQTPRGYLTSEMFNSTYKLYTHSYLGFGLKAARLATIAGALETE-GTGDGHTFASACLP 275
DB 269 LQASPPGYLTALRMENRTYKLYSYLGLGLMSARLAILGGVQPAKDGKELVSPCLSP 328
QY 276 WLEAEWIFGGVKYQYGGNQEVEGPEPCVAEVLVRVGRKLHQPBEVQSGSYAFSYYYDR 335
DB 329 SPKGEWEHAETVTRVSGQKAAASLHELCAARVSEVLQNRVHRTBEVKHVDYFAFSYYDL 388
QY 336 AVDTMDIDYKGGILKVEDFERKAREVCNLENFTSGSPFLCMLDSYITALLKDGFGFAD 395
DB 389 AAGVGLIDAEKGGSLVGDPEIAKXVCRTLETQPOSSPFCMDLTAVSLLLQGE-FGFPR 447
QY 396 STVQLTKKNNIETGALGATFHLLQSL 424
DB 448 SKVLKLTTRKIDNVETSWALGAIFHYIDSL 476

RESULT 7
Q8N3H3 PRELIMINARY; PRT; 503 AA.
AC Q8N3H3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein (Fragment).
GN DKF2761319.5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Amysala;
RA Ansonge W., Wirkner U., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL834158; CAD3864.1; -
DR InterPro; IPR000407; GDA1_CD39_NTPase.
DR Pfam; PF01150; GDA1_CD39; 1.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 503 AA; 54763 MW; 1639333F9139DBD9F CRC64;

Query Match 44.1%; Score 993; DB 4; Length 503;
Best Local Similarity 52.2%; Pred. No. 8.2e-77;
Matches 203; Conservative 55; Mismatches 125; Indels 6; Gaps 4;

QY 40 PINVSA---STLYGIMFDAGSTGTRIHYVTFVQKMPGQLPILGEVDFSVKPGLSAFVDQ 96
DB 109 PLGTAADGHEVYFGIMFDAGSTGTRVHVQFT-RPPRETPTLTHTFTKALPKGLSAYADD 167
QY 97 PQGAEITVQGLLEVAKDSIPRSHMKKTFWLKAATAGLRLPEHAKALLFEVKRSP 156
DB 168 VKSAQGIKRELLDVAKQDIPDFWKATPLVLKATAGLRLPEHAKALLQKVKVFRASP 227
QY 157 FLVPKGSVSIWQDEGIPFAMVTNVLFCQLHGRQETVGLDGGASTQITFLPQFEXT 216
DB 157 FLVPKGSVSIWQDEGIPFAMVTNVLFCQLHGRQETVGLDGGASTQITFLPQFEXT 216

RESULT 8
O76268 PRELIMINARY; PRT; 461 AA.
AC O76268;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NTPase protein (LD11641P).
GN NTPASE OR CG3059.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foaier C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush Z., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Khamel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lin Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,
RA Shue B.C., Siden-Klamis I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasmage D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh P.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
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QY 327 YAFSYDYDAVDTMIDYKGGILKVEDFERKAREVC--DNLENFTSGSPFLCMQLSYIT 384
DB 364 AAFSYFPERAIESGLVPLAGGETTVEAYRKAQEIICAIENDS-----QPFMCPDLTFFIS 418
QY 385 ALLKDGFGFADSTVLQTLTKVNNIETGALGATFHLLQS 423
DB 419 TLUREGFLNDGKIKIXIKYKDIGHGHSWALGCAYNVLTLS 457

RESULT 10
Q9XU84 ID Q9XU84 PRELIMINARY; PRT; 479 AA.
AC Q9XU84;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE K08H10.4 protein.
DE K08H10.4.
GN K08H10.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Periderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Gardner A.E.;
RL Submitted (Nov-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
RX EMBL: Z83113; CAB05544.1; -.
DR PIR: T23508; T23508.
DR WormPep; K08H10.4; C181877.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002034; AIPM/Hcit synth.
DR InterPro; IPR000407; GDAL_CD39_NTPase.
DR Pfam; PF01150; GDAL_CD39; 1.
DR PROSITE; PS00815; AIPM_HOMOCIT SYNTH 1; 1.
SQ SEQUENCE 479 AA; 5384 MW; 7EDC02A9D54A48ED CRC64;

Query Match 27.4%; Score 616.5; DB 5; Length 479;
Best Local Similarity 34.1%; Pred. No. 2.3e-44;
Matches 149; Conservative 82; Mismatches 167; Indels 39; Gaps 16;

QY 9 FFMVYS--CVCSAVSHRNQQTWFEGLFLLSMCPINVASSTLYGIMFDAGSTGTRTHVYT 66
DB 6 FSILLISFFLLSVVITTKTY-WCHGDGVLN---NQHTCRFTTVIDAGSTGTRHLHYK 60
QY 67 FVQK-----MFGQLPILGEVFDSPKGLSAFVDQPKQGAETVQGLLEVAKDSIPRSH 119
DB 61 FIHDPALASHGMPFK--VEKEIFQVKPGLSSFAKSPSSAADSLSPLQLQARKEVPHFM 117
QY 120 WKTPVVLKATAGLRLPEKAKALLFEVKE-IFRKSPLVLPKGSVIMTQDEGIFAWV 178
DB 118 WEXTPTLKATAGLRLPGDVAADDILESVEERIFNSGFFAAPPDAVNVMPGSEGVYSWF 177
QY 179 TVNFLTQLH-----GHR---QETVGTLDLGASTQITLPEKTELEOTPRGYLTSFE 229
DB 178 TMLLETLETFDFTVGHKPAARHSAVAAFGLGGSTQLTWPNNEAVFSEHV-GYERDID 236
QY 230 MFNSTYKLYTHSYLGFGLKAARLATIQALETG--TDGHTFRACLPRLLE-ABWLPFGV 286
DB 237 FFGHRLFLTHSFLNGLIAARLNIL-QLETDNEIEBTHQLITSCMPEGYQLTWEVY-AL 294
QY 287 KYOYGGNQEVEGFEPCYAEVLVWR-GKLHQPEEYQGRGSFYAFSYTYDRAVDTMDIYE 345
DB 295 KP-WNINGSSSHGFESCIGTKRWFVSSEIEMHRELKGSVYLFSTFFDRALNSGLVKN 353
QY 346 KGGILKVEDFERKAREVC-----DNLENFTSGSPFLCMQLSYITALLKDGFGFADSTVLQ 401
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DB 354 EGGKIELAQFKEAABACRRREKTEIDDDGSHMPWQCLDTYIYSLRDGYQFEDNQPLVL 413
QY 402 TKKVANNIETGVALGATF 418
DB 414 AKKIKMEVSVWGQGLAF 430

RESULT 11
Q8CHZ3 ID Q8CHZ3 PRELIMINARY; PRT; 278 AA.
AC Q8CHZ3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Similar to ectonucleoside triphosphate diphosphohydrolase 6.
GN ENTPD6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
RA Strausberg R.;
RL EMBL: BC038126; AAH38126.1; -.
DR MGI; MGI:1202295; EntpD6.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR000407; GDAL_CD39_NTPase.
DR Pfam; PF01150; GDAL_CD39; 1.
KW Hydrolase.
SQ SEQUENCE 278 AA; 30130 MW; 75A92DD1AC76297F CRC64;

Query Match 26.2%; Score 590; DB 11; Length 278;
Best Local Similarity 58.0%; Pred. No. 1.9e-42;
Matches 119; Conservative 29; Mismatches 51; Indels 6; Gaps 2;

QY 49 YGIMFDAGSTGTRIHVTFVQMPQQLPILGEVFDSPKGLSAFVDQPKQGAETVQGLL 108
DB 74 YGIMFDAGSTGTRIHVQFPA-RPPGETPLTHETFKALKPGLSAYADDVKSAGQIQELL 132
QY 109 EVAKDSIPRSHWKTTPVLKATAGLRLPEKAKALLFEVKEIFRKSPLVLPKGSVIMT 168
DB 133 NVAKQHIYPDFPKATPLVLKATAGLRLPEKAKALLQKVKVEVFKASPLVGGDCCVSN 192
QY 169 GDEGIFAWTVNFLTQLHGRHQRSTVGTLDLGASTQITLPEKTELEOTPRGYLTSF 228
DB 193 GTDEGVSAITVNFITSLKTPGSSSVGMLDGGSTQITLPRVEGTIQAAPPGLHTAL 252
QY 229 EMFNSTYKLYTHSYLGFGLKAARLA 253
DB 253 QMFNRTYKLYSYRWV-----CSRLA 272

RESULT 12
Q9UT35 ID Q9UT35 PRELIMINARY; PRT; 556 AA.
AC Q9UT35;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative guanosine-diphosphatase (Guanosine diphosphatase).
GN SPAC824.08 OR GD21.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OX Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972h-;
RA Barrell B.G.; Rajandream M.A.; Quail M.; Seegar K.; Harris D.;
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OM protein - protein search, using sw model

Run on:	July 1, 2004, 13:43:42 ; Search time 16.5 Seconds (without alignments) 2495.150 Million cell updates/sec
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Title: US-10-091-085-7
 Perfect score: 2252
 Ssequence: 1 MATSWGTVFFMLVVCVCSA.....ETGALGATFHLQLQSLGISH 428
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

```
Database :      PIR_78:*
1:  pir1:*
2:  pir2:*
3:  pir3:*
4:  pir4:*
```

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	616.5	27.4	479	2	T23508	hypothetical prote
2	535.5	23.8	556	2	T29109	probable guanidine
3	488.5	21.7	518	2	A40732	guanosine-diphosph
4	484	21.5	455	2	S48859	nucleoside triphos
5	441.5	19.6	454	2	JC4616	aprase (EC 3.6.1.
6	425.5	18.9	516	2	G84442	probable nucleosid
7	398	17.7	483	2	D86275	hypothetical prote
8	382.5	17.0	485	2	T34147	hypothetical prote
9	374.5	16.6	557	2	T16696	hypothetical prote
10	371	16.5	630	2	S50463	hypothetical prote
11	366	16.3	510	2	I56242	lymphoid cell acti
12	345	15.3	572	2	T40856	probable nucleotid
13	332.5	14.8	405	2	E86276	hypothetical prote
14	279	12.4	1052	2	T04439	hypothetical prote
15	242	10.7	508	2	C86275	7A19_33 protein -
16	148	6.6	628	2	A55421	nucleoside-triphos
17	108.5	4.8	1019	2	T40813	probable cell divi
18	106.5	4.7	535	2	F97910	glucan 1,6-alpha-g
19	105.5	4.7	553	1	G1BPSV	gene 1 protein - S
20	104.5	4.6	535	2	C95040	glucan 1,6-alpha-g
21	100.5	4.5	1151	2	H71347	hypothetical prote
22	99.5	4.4	774	2	T14555	DNA polymerase hom
23	99	4.4	711	2	S65749	hypothetical prote
24	99	4.4	726	2	AB0122	probable ferric si
25	98.5	4.4	427	2	PN0637	polyketide synthas
26	98	4.4	497	1	JC2192	subtilisin-like pr
27	96.5	4.3	287	2	T40138	probable ribosomal
28	96	4.3	477	2	JS0597	t-plasminogen acti
29	95.5	4.2	301	2	E71482	phosphatidylserine

hypothetical prote
Hs-transporting tw
hypothetical prote
probable serine/th
probable type II D
coproporphyrinogen
acetylornithine am
vrlt protein - Dic
hypothetical prote
patched protein -
hypothetical prote
cytochrome o ubiq
capsular polysacch
betaine aldehyde d
protein F3H2.4 (1
glycine hydroxymet

ALIGNMENTS

RESULT I

T23506
hypothetical protein K08H10.4 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C:Accession: T23508
R:Gardner, A.
Submitted to the EMBL Data Library, November 1996
A:Reference number: Z19750
A:Accession: T23508
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-479 <WIL>
A:Cross-references: EMBL:Z83113; PIDN:CAB05544.1; GSPDB:GN00023; CESP:K08H10.4
A:Experimental source: clone K08H10
C:Genetics:
A:Gene: CRSP:K08H10.4
A:Map position: 5
A:Introns: 36/3; 83/3; 189/1; 300/2; 412/3

Query Match	27.4%;	Score	616.5;	DB 2;	Length	479;			
Best Local Similarity	34.1%;	Pred. No.	7.3e-44;						
Matches	149;	Conservative	82;	Mismatches	167;	Indels	39;	Gaps	16;
QY	9	PFLMVS--CVCASVSHRNQQTWTFEGIFLSSMCPINVSASTLYGIMFDAGSGTGRTHVYT	66						
DB	6	PSILLISPSLLSVVTTKTQY-WCHGDDGLN---NQHTCRFFTVIDAGSGTGRLLHLYK	60						
QY	67	FVQK-----MPGOLPILEGRVFSVPSGLSAFVDQPKQAGATVQGLLEVAKDSIPRSH	119						
DB	61	RTHDPAIAASHGMFPK---VEKEIFQEVKPLSGSPAKSPSSAADSLLEPLQARKEVPHFM	117						
QY	120	WKKTVPVLKATAGTALLPEHKAKALLFEVKE--IPKSPPLVPKGSVIMTGODEGIFAWV	178						
DB	118	WEKTPITLTKATAGLTLGGDMADDLLESVEEIRFNSGFFAAFPDVAWVMPGSDGYSWF	177						
QY	179	TYNFLTGLH-----GHR---QETWGLDLGGASTQITFLPQPKTLEQTPRGYLTSFE	229						
DB	178	TLNILLETITDSEPTVGHKPAARHSAADFLLGGGTQLTYWPNNEAVPSEHV-GYERDID	236						
QY	230	MFNSTYKLYTHSYLGFGLKAAELATLGALETG--TDGHTFPSACLPLWLE-AEWTFGV	286						
DB	237	FEGHRIURLFTSHFLNGJIAAFNLIL-QLETDNEIESTHQLTSCMPEGYQVTEWBY-AL	294						
QY	287	KYQVGNQGEVGFPPCPYAEVLRVVR-GKLHQPEEVQORGSAFSPYYORAVDTMDIYE	345						
DB	295	KF-WNINGSSSHSPESCQVTTKNFVBSSEIWMHLRELKGPSVYLPSPVFPDRALNSGLVKGN	353						
QY	346	KGGILKVEDFERKAREVC-----DNLENTSGSPFLCMOLSYITALLKGQGFADSTVLQL	401						
DB	354	EGGKILQRFKEAABIAICREKTEIDDSGHMMPWQCLDITYLSLARDGYQFEDNQPLVL	413						

QY 402 TKKNNIETGKALGATP 418
DB 414 AKKINGMEVSGQGLAF 430

RESULT 2
T39109
Probable guanosine-diphosphatase - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T39109
R:Barrell, B.G.; Rajandream, M.A.; Quail, M.; Seegar, K.; Harris, D.
submitted to the EMBL Data Library, October 1999
A:Reference number: 221828
A:Accession: T39109
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-556 <BAR>
A:Cross-references: EMBL:AL121741; PIDN: CAB57338.1; GSPDB: GN000056; SPDB: SPAC824.08
A:Experimental source: strain 972h-; cosmid c824
C:Genetics:
A:Gene: SPDB: SPAC824.08
A:Map position: 1

Query Match 23.8%; Score 535.5; DB 2; Length 556;
Best Local Similarity 34.1%; Pred. No. 5e-37;
Matches 143; Conservative 61; Mismatches 158; Indels 57; Gaps 13;

QY 49 YGIMFDAGSTGTRCHVTEVQKMPGQLPILLEGVDSVKGLSAFVDPQKGAETVQGL 108
DB 134 YVLMIDAGSTGSRVHVQPNCFNS--PKLEEFKMEIEGLSFAQDPGAAASLDPLL 191

QY 109 EVAKDSIPRSHWKTTPVVKATAGLRLLPEHKAALLPEVKEIFRKS-PFLVPRKGSVIM 167
DB 192 DYAMENVEEYRRCSPIAVATAGLRLTGSEAKALKSVRQHLNDYPPFIVKDGVSIL 251

QY 168 TQDEGIFAWTVNFTLQGLHGH-ROETVGTDLGGASTGQITLPOFEKTELEQTPRG--- 223
DB 252 EGSMEGIYAMTINYLTLGGKATHSTVAVMDLGGASTQLVPEPRFASGESLVMDGDK 311

QY 224 YLTSFEMFNSTYKLYTHSYLGFGLKAARL-----ATLGALETEGTGHTFRSAC 272
DB 312 YVLDTN--GEQYELVQSHLGYGLKEARKLHKFVLNNAEALKESLELLG-DSTSIIHPC 368

QY 273 L-----PWLEAEWTFEGVQYQYGGNQBGEVGFBCYAEVLVR-----GKLRQP 318
DB 369 LHLNASLTHPDSKSEASEVVFVGPSSLAHLSLQCRGIAEKALYKDKNCPVRPCSFNGVHP 428

QY 319 ---EEVQKGSFYAPSYVYDRAVDTMDIDYEKGGILKVEDPERKAREVC----- 363
DB 429 KFTETFTDSPIYLSIYDR-----MISLGNPSTFTIEDMKYLANSVCSPTYWDQAFSL 493

QY 364 -DNLENFTSGSPFLCMDSYITALLKDGFGFADSTVLQTKKNNIETGHTFRSAC 421
DB 484 TDALKELKE-EPEWCLDLNTMISLLSVGYEIPNRRQLHTAKKIDNKBELGWLGLASLSML 541

RESULT 3
A40732
Guanosine-diphosphatase (EC 3.6.1.42) - Yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YEL042W
C:Species: Saccharomyces cerevisiae
C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 02-Sep-2000
C:Accession: A40732; B40732; S50502
R:Abelion, C.; Yanagisawa, K.; Mandon, E.C.; Hausier, A.; Moremen, K.; Hirschberg, C.B.;
J. Cell Biol. 122, 307-323, 1993
A:Title: Guanosine diphosphatase is required for protein and sphingolipid glycosylation
A:Reference number: A40732; MUID: 93308137; PMID: 8391537
A:Molecule type: DNA
A:Residues: 1-518 <ABE>
A:Cross-references: EMBL:L19560; NID: g349392; PIDN: AAA34656.1; PID: g349393

A:Note: sequence extracted from NCBI backbone (NCBIN:134708, NCBIP:134711)
A:Accession: B40732
A:Molecule type: protein
A:Residues: 125-144; 238-257; 276-281; 366-374; 399-412 <AB2>
R:Mulligan, J.T.; Dietrich, F.S.; Hennessey, K.M.; Sehl, P.; Komp, C.; Wei, Y.; Tayl
submitted to the EMBL Data Library, February 1993
A:Reference number: S30812
A:Accession: S30837
A:Molecule type: DNA
A:Residues: 1-518 <MUL>
A:Cross-references: GB:U18779; EMBL:L10830; NID: g603625; PIDN: AAB65000.1; PID: g60363
R:Dietrich, F.S.
A:Description: The sequence of S. cerevisiae cosmids 8199, 8334, and 9871.
A:Reference number: S50491
A:Accession: S50502
A:Molecule type: DNA
A:Residues: 1-518 <DIE>
A:Cross-references: EMBL:U18779; NID: g603625; PIDN: AAB65000.1; PID: g603637; MIPS: YEL
C:Genetics:
A:Gene: SGD: GDAL
A:Cross-references: SGD: S0000768; MIPS: YEL042W
A:Map position: 5L
C:Function:
A:Description: hydrolase
C:Superfamily: nucleoside triphosphatase chromatin-associated
C:Keywords: glycoprotein; Golgi apparatus; hydrolase; transmembrane protein
F:10-24/Domain: transmembrane #status predicted <TMM>
F:41,280,335/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 21.7%; Score 488.5; DB 2; Length 518;
Best Local Similarity 33.0%; Pred. No. 5e-33;
Matches 143; Conservative 56; Mismatches 159; Indels 75; Gaps 15;

QY 49 YGIMFDAGSTGTRCHVTEVQKMPGQLPILLEGVDSVKGLSAFVDPQKGAETVQGL 107
DB 93 YVLMIDAGSTGSRVHVQPNCFNS--PTLLDERFDMLEPGLSFDTSVGAANSLDPL 149

QY 108 LEVAKDSIPRSHWKTTPVVKATAGLRLLPEHKAALLPEVKEIFRKS-PFLVPRKGSVIM 165
DB 150 LKVAKYVTPIKARSTCPVAVKATAGLRLLGDAKSKILSAVRDHLKEDYPPFVVEGDGVS 209

QY 166 IMTQDEGIFAWTVNFTLQGL--HGHROETVGTDLGGASTGQITLPOFEKTELEQTPRG 223
DB 210 IMGDEEGVFAITNTYLLGNIGANGPKLPTAAVFDLGGSTQIVPEFPFPIKERNVDE 269

QY 224 YLTSFEMFNSTYKLYTHSYLGFGLKAAR-----LATLGALETEGTGHTFRSAC 272
DB 270 HKFDLKFGEENTYLYQPSHLGYGLKEGRKNVSVLVENALKDGKILKGDNTKTHQLSSPC 329

QY 273 LPRWLEA--EWI-----FGSVKYQYCG-----NORGEVGFEPCCYAEVL 309
DB 330 LPPKVNATNWKVILSKETTYTDFIGPDEPSGAQCRFLTDEILNKDAQCSPPCSF---- 385

QY 310 VVRGKLHQPPEV-----QRGSFYAFSYDRAVDTDM-IDYERGGILKVEDPERKAREVC- 363
DB 386 ---NGVHQPDSLVRTPKESNDIYFVFDYDTRPLGMLPSF-----TLNELNDLARI 436

QY 364 -----DNLENFTSGSPFLCMDSYITALLKDGFGFADSTVLQTKKNNIET 410
DB 437 GSETNWSVPSGAGSLDELSDSHP-CLDLSQVSLHTGTGDIPLQREURTKRKANKRI 495

QY 411 GWALGATPHLLQS 423
DB 496 GNCGLASLPLAKA 508

RESULT 4
S48859
nucleoside triphosphatase precursor, chromatin-associated - garden pea
C:Species: Pisum sativum (garden pea)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 29-Sep-1999
C:Accession: S65147; S48859

QY 402 TKKNNIETGKALGATP 418
DB 414 AKKINGMEVSGQGLAF 430

RESULT 2
T39109
Probable guanosine-diphosphatase - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T39109
R:Barrell, B.G.; Rajandream, M.A.; Quail, M.; Seegar, K.; Harris, D.
submitted to the EMBL Data Library, October 1999
A:Reference number: 221828
A:Accession: T39109
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-556 <BAR>
A:Cross-references: EMBL:AL121741; PIDN: CAB57338.1; GSPDB: GN000056; SPDB: SPAC824.08
A:Experimental source: strain 972h-; cosmid c824
C:Genetics:
A:Gene: SPDB: SPAC824.08
A:Map position: 1

Query Match 23.8%; Score 535.5; DB 2; Length 556;
Best Local Similarity 34.1%; Pred. No. 5e-37;
Matches 143; Conservative 61; Mismatches 158; Indels 57; Gaps 13;

QY 49 YGIMFDAGSTGTRCHVTEVQKMPGQLPILLEGVDSVKGLSAFVDPQKGAETVQGL 108
DB 134 YVLMIDAGSTGSRVHVQPNCFNS--PKLEEFKMEIEGLSFAQDPGAAASLDPLL 191

QY 109 EVAKDSIPRSHWKTTPVVKATAGLRLLPEHKAALLPEVKEIFRKS-PFLVPRKGSVIM 167
DB 192 DYAMENVEEYRRCSPIAVATAGLRLTGSEAKALKSVRQHLNDYPPFIVKDGVSIL 251

QY 168 TQDEGIFAWTVNFTLQGLHGH-ROETVGTDLGGASTGQITLPOFEKTELEQTPRG--- 223
DB 252 EGSMEGIYAMTINYLTLGGKATHSTVAVMDLGGASTQLVPEPRFASGESLVMDGDK 311

QY 224 YLTSFEMFNSTYKLYTHSYLGFGLKAARL-----ATLGALETEGTGHTFRSAC 272
DB 312 YVLDTN--GEQYELVQSHLGYGLKEARKLHKFVLNNAEALKESLELLG-DSTSIIHPC 368

QY 273 L-----PWLEAEWTFEGVQYQYGGNQBGEVGFBCYAEVLVR-----GKLRQP 318
DB 369 LHLNASLTHPDSKSEASEVVFVGPSSLAHLSLQCRGIAEKALYKDKNCPVRPCSFNGVHP 428

QY 319 ---EEVQKGSFYAPSYVYDRAVDTMDIDYEKGGILKVEDPERKAREVC----- 363
DB 429 KFTETFTDSPIYLSIYDR-----MISLGNPSTFTIEDMKYLANSVCSPTYWDQAFSL 493

QY 364 -DNLENFTSGSPFLCMDSYITALLKDGFGFADSTVLQTKKNNIETGHTFRSAC 421
DB 484 TDALKELKE-EPEWCLDLNTMISLLSVGYEIPNRRQLHTAKKIDNKBELGWLGLASLSML 541

RESULT 3
A40732
Guanosine-diphosphatase (EC 3.6.1.42) - Yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YEL042W
C:Species: Saccharomyces cerevisiae
C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 02-Sep-2000
C:Accession: A40732; B40732; S50502
R:Abelion, C.; Yanagisawa, K.; Mandon, E.C.; Hausier, A.; Moremen, K.; Hirschberg, C.B.;
J. Cell Biol. 122, 307-323, 1993
A:Title: Guanosine diphosphatase is required for protein and sphingolipid glycosylation
A:Reference number: A40732; MUID: 93308137; PMID: 8391537
A:Molecule type: DNA
A:Residues: 1-518 <ABE>
A:Cross-references: EMBL:L19560; NID: g349392; PIDN: AAA34656.1; PID: g349393

R:Shieh, H.L.; Tong, C.G.; Thomas, C.; Roux, S.J.
Plant Mol. Biol. 30, 135-147, 1996
A:Title: Light-modulated abundance of an mRNA encoding a calmodulin-regulated, chromatin
A:Reference number: S65141; MUID:96197404; PMID:8616230
A:Accession: S65147
A:Molecule type: mRNA
A:Residues: 1-455 <HS2>
A:Cross-references: EMBL:Z32743; NID:G563611; PIDN:CAA83655.1; PID:G563612
C:Superfamily: nucleoside triphosphatase chromatin-associated
C:Keywords: nucleus

Query Match 21.5%; Score 484; DB 2; Length 455;
Best Local Similarity 33.4%; Pred. No. 9.8e-33;
Matches 139; Conservative 62; Mismatches 161; Indels 54; Gaps 14;
QY 49 YGIMFDAGSTGTRIHYTFVQKMPGQPLILEG-EVFDVSKPGLSAFVDPQKQGAETVQGL 107
DB 44 YAVVFDAGSTGTRIHYTFVQKMPGQPLILEG-EVFDVSKPGLSAFVDPQKQGAETVQGL 102
QY 108 LEVAKDSIPRSHWKKTPVVLKATAGLRLPEHAKALLFEVKEIP-RKSPFLVPKGSVSI 166
DB 103 LEQAEVDPDLPKTPVRLGATAGLLENGDASEKILQSVRDMLSNRSTFVQPDVSI 162
QY 167 MTQDQSGIPAWVTNVELTQGLHGRHROETVGLDGGASTQITFLPOFEKTLBOTPR----- 222
DB 163 IDGTQSGYLWTVNVALNGLKYYTKTVGVIDLGGSVQMAVAS-KTKAKNAPKVDG 221
QY 223 --GYLTSFEMFNSTYKLYTHSYLGRGLKAAALATLGALETGTDGHTFSS--ACLPRWLE 278
DB 222 DPEYIKVVLKGPYDLYVHSYLHFGREASRAEILKL-----TPRSPNPLLGNFN 272
QY 279 AEWIFGVGYQYGGNGEGEVGFPCYAEVLVVRGKHLHPEEVQVQSGP----- 326
DB 273 GIYVSGEFGKATAYTSG-ANFNKCKNTIRKAL--KLNVPCPYQNCFTGGINWGGGNGQ 329
QY 327 ---YAFSYVDRAVDMDIDYKGG-ILKVEDEPKAREVCD-NLENFTSGSPFL----- 376
DB 330 KMLFASSTFFLPEDTGMDASTPFIILRPDIETKAKACALNFEDAKSTTFPDLKXNV 389
QY 377 ----CMLSVITALLXGDFGADSTVLQTKKVN-----IETGWLGAATFHLQSL 424
DB 390 ASYVCMDLIYQVLLVDGFLDPLQKITSKEIEYDAIVEAAWPLGNVAEISAL 445

RESULT 5
JC4616
N:Alternative names: precursor - potato
C:Species: Solanum tuberosum (potato)
C:Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 28-May-1999
C:Accession: JC4616; PC4147
R:Handa, M.; Guidotti, G.
Biochem. Biophys. Res. Commun. 218, 916-923, 1996
A:Title: Purification and cloning of a soluble ATP-diphosphohydrolase (Apyrase) from pot
A:Reference number: JC4616; MUID:96158985; PMID:8579614
A:Accession: JC4616
A:Molecule type: mRNA
A:Residues: 1-454 <HAN>
A:Cross-references: GB:U85897; NID:G1381632; PIDN:AA802720.1; PID:G1381633
A:Accession: PC4147
A:Molecule type: protein
A:Residues: 59-95/96-131/132-160/236-253/332-345 <HA2>
A:Experimental source: tubers
A>Note: The authors translated the codon GCA for residue 215 as Gly
C:Comment: This enzyme belongs to a family of E-type Apyrases, and it catalyzes the hydro
lyzed in starch synthesis.
C:Genetics:
A:Gene: rrop1
C:Superfamily: nucleoside triphosphatase chromatin-associated
C:Keywords: glycoprotein; hydrolase; transmembrane protein
F:1-30/Domain: signal sequence #status predicted <SIG>
F:8-25/Domain: transmembrane #status predicted <TM>

F:31-454/Product: ATP-diphosphohydrolase #status predicted <MAT>
F:44-65/Region: actin-heat shock protein 70-hexokinase beta-phosphate binding
F:192-212/Region: nucleotide binding #status predicted
F:192-212/Region: actin-heat shock protein 70-hexokinase gamma-phosphate binding
F:390-410, 427-446/Region: nucleotide binding #status predicted
F:151,262/Binding site: carboxylic (Asn) (covalent) #status predicted
Query Match 19.6%; Score 441.5; DB 2; Length 454;
Best Local Similarity 28.6%; Pred. No. 3.7e-29;
Matches 130; Conservative 78; Mismatches 178; Indels 69; Gaps 16;
QY 25 NOOTWFEIGIFLS-----SMCPINVS-----STLYGIMFDAGSTGTRIHY 65
DB 3 NONSHFIILAIPLVPLSLSKVNAQIPLRHLSSHSEHYAVIFDAGSTGSRVVP 62
QY 66 TPVQKPGQPLILEG-EVFDVSKPGLSAFVDPQKQGAETVQGLLEVAKDSIPRSHWKKTP 124
DB 63 RFDEKL-GLLPIGNINIEYFMATEPGLSSYAEADPKAAANSLEPLDGAEGVVPQELQSTP 121
QY 125 VVLKATAGLRLPEHAKALLFEVKEIP-RKSPFLVPKGSVSIIMTQDQSGIPAWVTNVL 183
DB 122 LELGATAGLRLKGAASKILOAVNLVKNQSTHRSKQNWITLDGTQSGSYMAAINYL 181
QY 184 TQGLHGRHROETVGLDGGASTQITFL--POFEKTL-OTPRGYLTSFEMFNSTYKLYT 239
DB 182 LGNLGKDYKSTTATIDLGGSVQMAVATSNQFAKAPQNEDEGPYVQCKHLSKDYNLV 241
QY 240 HSYLGFGLKAAALATLGALETGTDGHTFPRACLPWLEAWIFGVGYQYGGNGEGEVG 299
DB 242 HSYLNGQLAGRAEIFKASRNES-----NPCALEGCDGYSGYGVGVYKVPKPKGS-- 292
QY 300 FEPYAEVLVVRG--KLHPEEVQVQSGF-----YAFSYVDRAVDMDI 342
DB 293 ---SNKRCERLTHALKINAKNIEECFTFNGVWGGGDKGNHASSFFYDGAQVGIV 349
QY 343 DYE-KGGLKVEDEPKAREVCD-NLENFTS-----GSPFLCMLDLSYITALLKQDGF 392
DB 350 DTKFPSALAKPIQYLNAAKAVACQTNVADIKSIFFKTDQRNIPYLCMDLIYETILLVDGFG 409
QY 393 F---ADSVTLQTKKVN-IETGWLGAATFHLQSL 423
DB 410 LNPHEKITVHDVQKYLVGAAWPLGCAIDLVS 444

RESULT 6
G84442
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 18-Nov-2002
C:Accession: G84442
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.S.; Unayam, L.; Tallon
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Vente
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: G84442
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-516 <STO>
A:Cross-references: GB:AB002093; NID:G3461821; PIDN:AAC32915.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g02970
A:Map position: 2
C:Superfamily: nucleoside triphosphatase chromatin-associated
Query Match 18.9%; Score 426.5; DB 2; Length 516;
Best Local Similarity 30.4%; Pred. No. 8.2e-28;
Matches 126; Conservative 63; Mismatches 153; Indels 73; Gaps 13;
QY 42 NVSASTLYGIMFDAGSTGTRIHYTFVQKMPGQPLILE-GEVFDVSK--PGLSAPVDQ 97

```
Db 61 NLRGSLRYSVVLDGGSTGTRIHVFGY--RIESGKPVFFPRGANYASUKLHPGLSFAFDDP 118
Qy 98 KQAGETVQGLLEVAKDSIPRSHWKKTPVVLKATAGLRLPEHRAKALLFEVKIFRKSPP 157
Db 119 DGASVSLTELVEFAKVRPKGMWLETVEVLWATAGMLLELPVQEKILGVARRVLKSSGP 178
Qy 158 LVPKGSVINTGQDEGIFAMVTVNFTGLQHLGHRQETVGTLDIGGASTQTTPFL-----P 211
Db 179 LFRDEWASVIGSGDEGVYAWYANFALGSLGGDFLKTGTGIVELGGASAQVTFVSSEMPMP 238
Qy 212 QFEKTELETPRGYLTSPFEMENSTYKLYTHSYLGLGKAAARLATLGAAL-----ETRGTD 264
Db 239 EFSRTI-----SFG--NVTNLYSHSFHFGQNAADKLGWLLSRDCHNSAVEPTR 287
Qy 265 GHTFRSACLPR-----WLEAEWTFGGVQYQYQGNQGEVGFPCYAEVURV 311
Db 288 EKIFTPCAPKGYNDANTQKLSGLLAESRLSDSPQAGCN-----YSQCRSAALTIL 341
Qy 312 RGKLRQPEVQVGSFYAFSYDDRAVDTDMI-----DYEGGILKVEDPERKAREV 362
Db 342 QDGNRILIIITAGSFIFFGLEGKAWUSIMFASGERFGEDWSK---LRVADPSLHREDL 398
Qy 363 CDNLENFTSGSPFLCMLDSYITALLKQGFPG-ADSTVLQUTKKNVNTISTGAWLGA 416
Db 399 LR-----YCFSSAYIVSLHDTLGIPLDDEIRIGYANQAGDIPLDWALGA 442

RESULT 7
D86276
hypothetical protein P7A19.34 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 18-Nov-2002
C:Accession: D86276
R:Theologos, A.; Becker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cresay, T.H.; Dewar, K.;
Nasser, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
Xer, M.; Wu, D.; Xu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: D86276
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-483 <STO>
A:Cross-references: GB:AE005172; NID:95080801; PIDN:AAD39311.1; GSPDB:GN00141
A:Map position: 1
C:Genetics:
C:Superfamily: nucleoside triphosphatase chromatin-associated

Query Match 17.7%; Score 398; DB 2; Length 483;
Best Local Similarity 27.4%; Pred. No. 1.9e-25;
Matches 119; Conservative 73; Mismatches 161; Indels 82; Gaps 17;

Qy 32 GFLSSMCPINVASLYGIMPDAGSTGTRIHV--YTFVQKPGQLPFILEGEVFD-----84
Db 59 GSLLSRCKLA-----YSVLIDAGSGSTRVHVFGESEKP-----VEDFGEKH 103
Qy 85 ----SVKPGLSAFVDPQKQAGETVQGLLEVAKDSIPRSHWKKTPVVLKATAGLRLPEHK 140
Db 104 YANLKLTPGLSSYADNPAGASVTKLVPEPAKQIPKRMFRSDIRLMATAGMMLLEVPV 163
Qy 141 AKALLFEVKEIFRKSPPFLVPRKGSVINTGQDEGIFAMVTVNFTGLQHLGHRQETVGTLDL 200
Db 164 QEQLIVTRVLRSSGFWRDEWANNVIGSGDEGLYSMTANYALGSLGTDPLETGVIEL 223
Qy 201 CGASTQTITLFPQFQKTLQTPRGYLTSPFEMENSTYKLYTHSYLGLGKAAARLATLGALET 260
Db 224 CGASAQVTFV-----SSEHVPFYSRTIAYGNISYTIYSHSFIDYGDAAALKKLEKLN 278

RESULT 8
T34147
hypothetical protein C33H5.14 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 17-Mar-2000
C:Accession: T34147
R:Bradshaw, H.; Stellyes, L.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid C33H5.
A:Reference number: Z21482
A:Accession: T34147
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-483 <BRA>
A:Cross-references: EMBL:U41007; PIDN:AAA82272.1; CESP:C33H5.14
A:Experimental source: strain Bristol N2
A:Genetics:
A:Gene: CESP:C33H5.14
A:Introns: 22/1; 83/1; 120/2; 167/1; 269/3; 399/3
C:Superfamily: nucleoside triphosphatase chromatin-associated

Query Match 17.0%; Score 382.5; DB 2; Length 485;
Best Local Similarity 27.5%; Pred. No. 3.8e-24;
Matches 119; Conservative 84; Mismatches 153; Indels 77; Gaps 18;

Qy 49 YGIMPDAGSTGTRIHVYTFVQKPGQLPFILEGEVFD-----VKPGLSAFVDPQKQAE 102
Db 25 YGVICDAGSGSTRLFVYT-LKPLSGGLTNIDTLIHSESEPVVKKVTPGLSGFKDPQVVE 83
Qy 103 TVQGLLEVAKDSIPRSHWKKTPVVLKATAGLRLPEHRAKALLFEVKEIFRKSPPFL-VPK 161
Db 84 YITPLRFAEHLIPYQLGETDLIIPATAGMLLPEAKDAIKMLONGLKSVTALRVSD 143
Qy 162 GSVSINTGQDEGIFAMVTVNFTGLQHLGHRQETVGTLDIGGASTQTITLFPQPEK-----215
Db 144 SNRIIDGAWEGYISVIYVNIILGRPDENDSKVGMIDMGASVQIAFIANEKESYNGG 203
Qy 216 TLEQTPRGYLTSPFEMENSTYKLYTHSYLGLGKAAARLATLGALETGDTGHTFRSACLPR 275
Db 204 NYVEINLGSITNEDTK--YKIYSTITFLYGANEGLKLYENSLVKSNS-----NDSCSPR 257
Qy 276 WLEAEWTFGGVQYQYQGNQGEVGFPCYAEVLRVVRGKLHOPE-----319
Db 258 GLNR--LIG-----EFTVNGTG--WDVCLAQVSSLI-GDKAQPSCNPTCFLRNVIAPSV 308
Qy 320 EVORGSGFYAFS--YYDRAVDTDMIDYEKGLKLVDPFERKAREVC-----DNLENFTSGSP 374
Db 309 NLSTVOLYGFSEYWTTS-----NFGSGGEYHYQKFTDEVRYKQKQWMDIQDGFKRNE 362
Qy 375 F-----LCMDLSYITALLKQGFPGFADST--VLQUTKKNVNTISTGAWLGA-----416
Db 363 FPNADIERLGTNCFKAAWTVSLHDGFN-VDXTKHLFQSVLKIAGEKQWALGAMLVHYSK 421
Qy 417 --TFHLLQSLGIS 427
Db 422 DLKENTLEQLEVA 434
```

RESULT 9

T16696
hypothetical protein R07B4.4 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C/Accession: T16696
R/Miller, N.
submitted to the EMBL Data Library, October 1995
A/Description: The sequence of C. elegans cosmid R07B4.
A/Reference number: Z19561
A/Accession: T16696
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-557 <MIL>
A/Cross-references: EMBL:U39652; NID:g1049390; PID:g1049394; PIDN:AAA80403.1; CESP:R07B4
A/Experimental source: strain Bristol N2
C/Genetics:
A/Gene: CESP:R07B4.4
A/Introns: 39/1; 67/1; 145/2; 192/1; 244/3; 317/3; 451/3; 486/2

Query Match 16.6%; Score 374.5; DB 2; Length 557;
Best Local Similarity 28.3%; Pred. No. 2.2e-23;
Matches 126; Conservative 70; Mismatches 159; Indels 91; Gaps 21;
QY 49 YGIMPDAGSTCTRIHYVTFVQKMPGQLPILGEVFDSD-----VKQCLSAFYVDQKQAE 102
DB 44 YGVICDAGSTGTLFLVNWISTSDSELTQIEPVYDNKPVKKISPLGLSTFGTKPAQAAE 103
QY 103 TVQGLLEVAKDSIPRSHWKTTPVVLKATAGLRLLPEH-----KAKALLPEVKEIFRKSPP 157
DB 104 YLRPLMELABRHPEEKRPVTFVIFATAGWRLLPDEYVLIGQKEAVL-----KNLRNKLPK 160
QY 158 L-----VPGKSVSMTGQDEGIFAWTVNFLTQGLH-----GH-RQTVGTLDL 200
DB 161 ITSMOVLKEHRIIEGKWEIGYIAVYALGKFNKTATLDPPCTSPAHARQKTGVGMDM 220
QY 201 GGASTQITP-LPOFEK-----TLEQTPRGYLTSEFMNSTYKLVTHSVLGF-----GLKAAR 251
DB 221 GGASQAIAFELPTDSESSINVENINLGCRDSDLFK-YKLFVTFYLGYGVNEGIRKYE 278
QY 252 LATIGALTEGTGHTFRSACLPRWLEAEWIFGKVQYQGN--QEG----- 296
DB 279 HMLSLKLKQD--NGTVIQDDCMPLNLHKT-----VTLNGENFVRGTGNWNTCSNEVKK 331
QY 297 ----EVCFEPCYAEVLVRVWVKLHOPE-EVQKGSFYAFSYVYDRAVDTMDIDYKESGLK 351
DB 332 LIMPSSSEVCKAEAKCYFGAVPAPSPILSNIMYGFSEYWTSTEDV-----LGLGQYD 387
QY 352 VEDFERKAREVCD-----NLENFTSGP-----FLCMDSLYITALLKDGFGFADST 397
DB 388 AENIAKKTQYCSKRWSTIQAESKKQLYPRADSERLNTQCFKSAWITSVLHDGFS-VDKT 446
QY 398 --VLQUTKKNVNIETGHALCA-TFHL 420
DB 447 HNRKFSYSTIAGQEVQWALGAMTYHM 472

RESULT 10

S50463
hypothetical protein YER005w - yeast (Saccharomyces cerevisiae)
C/Species: Saccharomyces cerevisiae
C/Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 19-Apr-2002
C/Accession: S50463
R/Dietrich, F.S.
submitted to the EMBL Data Library, December 1994
A/Description: The sequence of S. cerevisiae cosmids 9537, 9581, 9495, 9867, and lambda
A/Reference number: S50433
A/Accession: S50463
A/Molecule type: DNA
A/Residues: 1-630 <DIE>
A/Cross-references: EMBL:U18778; NID:g603592; PID:g603597; GSPDB:GN00005; MIPS:YER005W

C/Genetics:
A/Gene: SGD:YND1; MIPS:YER005W
A/Cross-references: SGD:S0000807
A/Map position: 5R

Query Match 16.5%; Score 371; DB 2; Length 630;
Best Local Similarity 26.0%; Pred. No. 5.2e-23;
Matches 116; Conservative 75; Mismatches 164; Indels 92; Gaps 17;
QY 49 YGIMPDAGSTGTRIHYVTF-----VQKMPGQLPILGE-----VFDSEVQGLSA 92
DB 10 FGIIVDAGSGSRHIVFKWQDTESLHATNQDSQILQSVPHIQEKDWT-F-KLMPGLSS 68
QY 93 FVDQPKQAEF-VQGLLEVAKDSIPRSHWKTTPVVLKATAGLRLLPEHKAALLPEV-KE 150
DB 59 PEKKFQDAYKSHIKELLDFAKNIIPESHWSSCFVTIQATAGWRLLPQDIQSSILDLGCG 128
QY 151 IPRKSPFLVP--KGSVSMTGQDEGIFAWTVNFLTQGLHGRQE-----TVGTLLDLGA 203
DB 129 LKHPAEFLVEDCSAQIQVIDGSETGLYGLWGLNLYLGHFNDPNPSVDHFTFGPMDMGA 188
QY 204 STQITFLPQPEKTLB-----QTPRGYLTSEFMNSTYKLVTHSYLGLPKKAEAL 252
DB 189 STQIAFAPDSGEIAHRDDIATIFLRSVNGDLQKQWDFVST-----WLGFGANQAR 241
QY 253 ATLGAL-----ETEGTDGHTFRSACLPRWLEAEWIFGKVQYQGNQEGEVGPE 301
DB 242 RYLAQLINTLPENTVDYENDPSTENLNDPCMERGSSTDFEFDKTFIAGSGNYEQCTK 301
QY 302 PCYAEVLR-----VVRGKLHOPE-EVQKGSFYAFSYVYDRAVDTMDIDYKESGLK 352
DB 302 STYPLLLKNMPDDEPCLFNGVHAPRIDFANDKFIGTSEYWTANDV-----FKLGSEYNF 357
QY 353 EDPERKAREVCN-----LENFTSG-----SPFL-----CMDSLYITALLKDGFGPA--- 394
DB 358 DKFSKSLREFCNSNTQILANSKGYNSIPENFLKDACFKGNWLVNILEGFDMPRIDV 417
QY 395 -----DSTVLQUTKKNVNIETGHALG 415
DB 418 DAENVNDRPLFQSVKEKVERELSWTLG 444

RESULT 11

I56242
lymphoid cell activation antigen - human
C/Species: Homo sapiens (man)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Nov-2002
C/Accession: I56242
R/Malczewski, C.R.; Delespesse, G.J.; Schoenborn, M.A.; Armitage, R.J.; Fanslow, M.
J. Immunol. 153, 3574-3583, 1994
A/Title: The CD39 lymphoid cell activation antigen. Molecular cloning and structural
A/Reference number: I56242; MUID:95015846; PMID:7930580
A/Accession: I56242
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-510 <RES>
A/Cross-references: GB:I573813; NID:g765255; PIDN:AA832152.1; PID:g765256
C/Superfamily: nucleoside triphosphatase chromatin-associated

Query Match 16.3%; Score 366; DB 2; Length 510;
Best Local Similarity 28.2%; Pred. No. 1e-22;
Matches 125; Conservative 72; Mismatches 172; Indels 74; Gaps 19;
QY 32 GTFPLSMCPINTVASTLYGIMFDAGSTGTRIHYVTFVQKMPGQLPILGEVFDSEVYK-PGL 90
DB 36 GLTONKALPENVK-----YGVILDAGSSHTSLYIKWPAEKENDTGVVHVQVBCRVGPGI 91
QY 91 SAFPVQPKQGAETVQGLLEVAKDSIPRSHWKTTPVVLKATAGLRLL-----PEHKAALLPE 147
DB 92 SKFVQKVNIEIGLYLTDCHERAREVIFRSQHSQSTPYLGTAGWRLLMESEELADRVLDV 151
QY 148 VKEIFRKSPLVPKGSVSLMTGDSGIFAWTVNFLTQGL-----HGRQFTV 195

Db 152 VERSLNNPFF--DFQGAIRITGQHEGAYGWITNYLLGKFSQKTRFSPVVPYETNNQETTF 209
QY 196 GTLDLGGASTQITFLPQFEXKLTQTPRGYLTSPFEMFNSTYKLYTHSYLGKKAARLATL 255
Db 210 GALLDGGASTQITFLPQFEXKLTQTPRGYLTSPFEMFNSTYKLYTHSYLGKKAARLATL 266
QY 256 GALTETGDTGHTFESACL-----PMLAEWIFGGVKYQVGGNQE 297
Db 267 -AKDIQVASEILLDPCHFPGYKVVVNSLYTKTPCKTFEMTLPQFQEIQIGN---- 321
QY 298 VGFPCYARLV-----VRGKLHQPEEVQSGFYAFSYYYDRAVDTMIDYE 345
Db 322 --YQCHQSILELNTSYCPYSCAFNGIFLPPLQGDGFAFSAP--YFVKKFLN---LTSE 375
QY 346 KGGILKYVEDPERK-AREVCNLENFTSG--SPFL---CMLSLVITALLKDGFGF-ADS-T 397
Db 376 KVSEKTEEMKFKCAQWSEIKTSYAGVKEKYLSEYCSGTVILSLILQGHYFTADSWE 435
QY 398 VLQTKKNNIETGWAIGATFHL 420
Db 436 HIHPIGKIQSDAGWTGLYMLNL 458

RESULT 12

T40856

Probable nucleotide phosphatase - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T40856

R:Ramsperger, U.; Pohl, T.; Wood, V.; Rajandream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, October 1999

A:Reference number: 221952

A:Accession: T40856

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-572 <RAM>

A:Cross-references: EMBL:AL121783; PIDN:CAB57847.1; GSPDB:GN00068; SPDB:SPCC11E10.05C

A:Experimental source: strain 972h-; cosmid c11E10

C:Genetics:

A:Gene: SPDB:SPCC11E10.05C

A:Map position: 3

Query Match 15.3%; Score 345; DB 2; Length 572;
Best Local Similarity 25.3%; Pred. No. 7e-21;
Matches 114; Conservative 69; Mismatches 156; Indels 112; Gaps 16;

QY 49 YGIMFDAGSTGTRTHVYTF-----VQKMPGOLPILGEVFD-----SVKPKLSAFVD 95
Db 5 YGIFIDAGSGSRLLIISWDYDTSLSLSDKVKKLPLEITGIGDGRKWSLKVQPGISSFAN 64
QY 96 QPKQ-GAETVOGLLEVANDSIPRSHMKTPVVLKATAGURLL-PEHKAALLFEYKBIPIR 153
Db 65 NPKHVGKGLKELLDFAHAIPKDVHKEFVFLSATAGNELLGVDQAKILSHACKYIKK 124
QY 154 KSPFLVP--KGSVSIMTQDEGIFAMVTVNLTGQLHGRQETVGTLDLGGASTQITFLP 211
Db 125 NYDFDIINCNSIRVIDGKAGMGMVGLATYLLKTLBKDTSTVGLDMGASVQIAP-- 182
QY 212 QFKETLSQTPRGVYTSFEMFNST-----YKLTHSYLGKKAARLATLGAAL- 258
Db 183 -----ELPPSOLKATYKDSISTVHIGLQNGQGLYPLFVTTWLGFCANEAYRVLGLLI 235
QY 259 ETE-GTQDHTFRSACLPRLEASWIFGGVKYQVGG-----NOGEVGFPCY 304
Db 236 ESENGKVGNTLSDPCSIR--GRYDIDGIEFAGTGDLKQCLKLYNLNKKDPCSNDFCN 293
QY 305 AEVLVRVGRKGLHQPEEVQSGFYAFSYYYDRAVDTMIDYEKGLIKVEDPERKAREVC- 363
Db 294 PDGISI-----PPVDPANTEFVGVSEFTYTTNDV-----FDMGSGYHFNFKYKVDYCG 343
QY 364 -----DNLENFTSGPFLQWLSVITALLKDGFGFADSTV---- 398
Db 344 TEWETMLSRNLNKLTFTSTENKLEK-----LCFKASWALNVLHGEFDVPSKNTSSND 396

RESULT 14

T04439

hypothetical protein T10816.150 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999

C:Accession: T04439

R:Bevan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansoorge, W.; Bancroft, I.; Mewes,

submitted to the Protein Sequence Database, April 1998

A:Reference number: Z15359

QY 399 -----LQTKKNNIETGWAIG 415
Db 397 AKDGLSVIPAYHSPFTSLEKIERTEVSWTLG 427

RESULT 13

E86276

hypothetical protein F14117.1 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001

C:Accession: E86276

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Ali

Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Iarov, J.S.; Maiti, R.; Marzi

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tall

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: E86276

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-405 <STO>

A:Cross-references: GB:AB005172; NID:97262666; PIDN:AAF43924.1; GSPDB:GN000141

C:Genetics:

A:Map position: 1

Query Match 14.8%; Score 332.5; DB 2; Length 405;
Best Local Similarity 26.3%; Pred. No. 4.8e-20;
Matches 110; Conservative 64; Mismatches 157; Indels 87; Gaps 15;

QY 48 LYGIMPAGSTGTRIHVYTFVQKQPLPILGEVFDSPKVLGSAFVQPKQGAETVQGL 107
Db 3 VFGYWPESGKP-----VFDFGSHYASL-----KLSPLGSSYADNPEGASVSVTKL 48
QY 108 LEVAKDSIPRSHMKTPVVLKATAGURLLPEHKAALLFEYKBIPIKSPFLVFKGVSIM 167
Db 49 VEPAGKIPKGLKSDIRLMATAGNELLDPVQEQILDTVRVLEASSGFKQDEWATVI 108
QY 168 TQDDEGIFAMVTVNLTGQLHGRQETVGTLDLGGASTQITFLPQPEKLTQTPRGYLS 227
Db 109 SGTDEGIYAVVAVNHALGSLGSDPLKTTGTIVELGGASAOVTFVPS-----EHVPPBSFRT 163
QY 228 PERFNSTYKLYTHSYLGKKAARLATLGALETE---GTQDHTFRSACLPR----- 275
Db 164 ISYGNVSTIYSHSFLDPQDAAEDKLLSLQNSVAASTGDGIVEDPCTPKGYIYTHSQ 223
QY 276 -----WLEAEWIF--GGVKYQVGGNQEVEGFGFPCYAEVLVRVVR--GKHLHQPEEVQSGFYA 328
Db 224 KDSGGLSBSSEKFKASLQVQAAGD-----FTKCRSATLAMLQEGKEN----- 265
QY 329 PSVYVDRAVDTMIDYEKGLIKVEDF-----ERKAREVCMDNL 366
Db 266 -CAVHCISGISTTPNIOGSLFATENFFHTSPFGKEKEWSEMLAGKRCFGEWSKL 324
QY 367 -ENF-TSGSPFL---CMLSLVITALLKDGFGPA-DSTVILQTKV--NNIETGWAIGA 416
Db 325 KEKYPTTKYLYTHSYLGKKAARLATLGALETE---GTQDHTFRSACLPR----- 382

Query Match 10.7%; Score 242; DB 2; Length 508;
Best Local Similarity 23.2%; Pred. No. 2.8e-12;
Matches 109; Conservative 78; Mismatches 161; Indels 122; Gaps 21;
QY 12 LVVSCVCSAV-----SHRNOQTWFEIGIPUSSMCPINVSASTLYGIMFDAGSTOT 60
DB 35 VIVACVTIAGLGLLIFIGYSILRSRNR-----VSLHYSVIIDGSSSGT 77
QY 61 RIHYVTFVQKMPGQLPIL-GEVDSVK--PGLSAFVDQPKQGAETVOGLLEVAKDSIP 116
DB 78 RVHVFY--RIESGRPVDFGBENTASUKLSPGLSAYADNPGVSESUTELVEFAKRVH 135
QY 117 RSHWKTTPVVLKATAGLRLLPEHKAKALLFEVKEIFRKSPPPLVPKGSVIMTQDDEGIFA 176
DB 136 KGLKAKSDIRLMATAGMLLELPVQEQILDVTRVLRSSGF-----DFRDE---- 181
QY 177 WYVNFPLGQLHGHQETVGTLDG-----CASTQITLPOFEXTLQOTPRGYLTSPM 230
DB 182 WASV---ISSEILENFDLAKVYMLGLLIMRSVRLEVFV-----STELVPSEFRTLAY 233
QY 231 FNSTYKLYTHSYLGFGLKAARLATIGAL---ETECTDGHTRFASACLPRWLEMI---- 282
DB 234 GNVSYNLISHFLDFGQDAQCKLSSLYNSAANSTGSGIVDPDPCIPKGYILETNLQKDL 293
QY 283 --PGVKYQYQGNQGEVGFPCYAEVLVRV-----GKLHQPVEVORGSTY 327
DB 294 PGFLADKGTATLQAGNFSECSAFAFMLEQEEKKCTYKRCSTGSIPTFN--LQGSFL 351
QY 328 AFSYVY-----DRAVDTDMI-----DYEKGILKVBDFPERKAREVCNLENF 369
DB 352 ATENEFHTSKFPGLGEKEMSEMILAGKFCPEEHSK---LKVYPTPKD-----ENLLRY 404
QY 370 TSGSPFLCMDSYITALLKQDGFPA-DSTVLQITKKV--NNIETGWALGA 416
DB 405 -----CPSSAYIISMLHSLDGLVALDDERIKYAKAGEEDIPLDWALGA 447

Search completed: July 1, 2004, 13:49:26
Job time : 17.5 secs

A;Accession: T04439
A;Molecule type: DNA
A;Residues: 1-1052 <BEV>
A;Cross-references: EMBL:AL021687
A;Experimental source: cultivar Columbia; BAC clone T18B16
C;Genetics:
A;Map position: 4
A;Intons: 79/3; 118/3; 217/1; 295/3; 396/3; 531/2; 815/3
A;Note: T18B16-150
Query Match 12.4%; Score 279; DB 2; Length 1052;
Best Local Similarity 25.1%; Pred. No. 6.2e-15;
Matches 108; Conservative 70; Mismatches 170; Indels 82; Gaps 19;
QY 51 IMPDAGSTGRHVV--TFVQKMPGQLPIL-----EGEVFD--SVKPGLSAFV 94
DB 525 LVIVITGTRAVYQASINYYKDDSLPIVWKSLETSRKSRCRAYDRMETEPGPKLV 594
QY 95 DQPKQGAET-VOGLLEVAKDSIPRSHWKTTPVVLKATAGLRLLPEHKAKALLFEVKEIFR 153
DB 585 NN-RTGLKTAIKELIQAWEKQIPKNAHRTTSLFWATAGVRRLRPADSSWILGNWSILA 643
QY 154 KSPFLVPKGSVIMTQDEGIPAWVTNFLTGLHG-HRQETVGTLDGASTQITFLPQ 212
DB 644 KSPFCRRREWKLIISGTEAYFCNTALNYOTSMGLALPKATFGALDGLGSSLQVTFENE 703
QY 213 FEXTLEQTTPRGYLTSPMFNSTYKLYTHSYLGFGLKAA-----RLATL----- 255
DB 704 -ERTHNETN---LNLRIQSVNHLGAYSLAGYGLNADPRS VVHLLKPLNWKSDLIE 758
QY 256 GALETGTGHTFRSACLPRWLAEWIFGCVKYQYQGNQGEVGFPE-----PCYAEVLVR 309
DB 759 GKLE-----MKHPCNLNSYNGVQYICQSCASSVQGGKKGSGVSIKLWAPNNGECSA 810
QY 310 VVR-GKXHOPEEVR--GSPAFSYTYDRAVDTDMDYKGGI--LKVEDPERKAREVC 363
DB 811 LAKNARCALPDGYPRHGQYAVSGPF-----VVYRPNLSAASLDDVLEKREFC 862
QY 364 DN-----LENPTSGSPFL---CMDLSYITALLKQDGFADSTV-----LQITKKVNIET 410
DB 863 DKAWQVARTSVSPQPTIEQCFRAPYIVSLREGLYITDKQIIIGSGSITWTLGVALLES 922
QY 411 GWALGATFHL 420
DB 923 GKALSITLGL 932

RESULT 15
C86276
7A19.33 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 18-Nov-2002
C;Accession: C86276
R;Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.P.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: C86276
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-508 <STO>
A;Cross-references: GB:AE005172; NID:G5080800; PIDN:AAD39310.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1
C;Superfamily: nucleoside triphosphatase chromatin-associated

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 1, 2004, 13:42:31 ; Search time 10 Seconds
(without alignments)
2228.603 Million cell updates/sec

Title: US-10-091-085-3
Perfect score: 2250
Sequence: 1 MATSWGVFVFLVVCVCSA.....ETGVALGATFHLQSLGISH 428

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2250	100.0	428	1 ENP5_HUMAN	Q75356 homo sapien
2	1994.5	88.6	427	1 ENP5_MOUSE	Q9wuz9 mus musculus
3	1933.5	85.9	429	1 ENP5_MESAU	Q9qyc8 mesocricetu
4	999	44.4	484	1 ENP6_HUMAN	Q75354 homo sapien
5	986	43.8	455	1 ENP6_RAT	Q9er31 rattus norv
6	489	21.7	455	1 NTPA_PEA	P52914 pisum sativ
7	483.5	21.5	518	1 GDAL_YEAST	P32621 saccharomyc
8	446.5	19.8	454	1 APY_SOITU	P80595 solanum tub
9	387.5	17.2	485	1 YB4_CAEEL	Q18411 caenorhabdi
10	385	17.1	552	1 YB4_CAEEL	Q21815 caenorhabdi
11	383	17.0	493	1 ENP1_CHICK	Q93295 gallus gall
12	372	16.5	630	1 YND1_YEAST	P40009 saccharomyc
13	370	16.4	510	1 ENP1_MOUSE	P55772 mus musculu
14	365	16.2	513	1 ENP1_BOVIN	Q18956 bos taurus
15	360.5	16.0	612	1 ENP4_MOUSE	Q9dbt4 mus musculu
16	357	15.9	616	1 ENP4_HUMAN	Q9y227 homo sapien
17	352	15.6	510	1 ENP1_PIG	Q9myu4 sus scrofa
18	351	15.6	510	1 ENP1_HUMAN	P49961 homo sapien
19	348.5	15.5	511	1 ENP1_RAT	P97687 rattus norv
20	347.5	15.4	529	1 ENP3_HUMAN	Q75355 homo sapien
21	339.5	15.1	495	1 ENP2_HUMAN	Q9y213 homo sapien
22	309.5	13.8	495	1 ENP2_MOUSE	C55026 mus musculu
23	302.5	13.4	495	1 ENP2_RAT	C55795 rattus norv
24	301.5	13.4	494	1 ENP2_CHICK	P79784 gallus gall
25	140	6.2	628	1 NTP1_TOXGO	Q27895 toxoplasma
26	138	6.1	628	1 NTP2_TOXGO	P52913 toxoplasma
27	131	5.8	592	1 NTP4_TOXGO	Q46455 moorella th
28	111.5	5.0	634	1 SELB_WOOTH	P11333 spiroplasma
29	106.5	4.7	553	1 VGL1_SPV4	Q05470 bacillus su
30	104.5	4.6	4427	1 PKSL_BACSU	O83273 treponema p
31	101.5	4.5	1151	1 Y245_TREPA	Q54796 streptococc
32	99.5	4.4	535	1 DEXB_STRPN	P06874 bacillus st
33	99.5	4.4	548	1 THER_BACST	

34	97	4.3	1220	1	PTC1_BRARE	Q98864 brachydanio
35	96	4.3	711	1	DDP3_YEAST	Q08225 saccharomyc
36	95.5	4.2	2076	1	PAS1_YARLI	P34229 Y fatty aci
37	93	4.1	969	1	PAC4_HUMAN	P29122 homo sapien
38	93	4.1	1696	1	ITM2_HUMAN	Q9nm33 homo sapien
39	92	4.1	290	1	HEN6_CAUCR	Q9ast8 caulobacter
40	91	4.0	417	1	GLYA_BORBU	O51947 borrelia bu
41	91	4.0	477	1	URTI_DESSO	P98119 desmodus ro
42	90.5	4.0	301	1	PSD_CHLTR	O84705 chlamydia t
43	90	4.0	434	1	YFEW_ECO57	Q8xbj0 escherichia
44	90	4.0	434	1	YFEW_ECOLI	P77619 escherichia
45	89.5	4.0	601	1	SYR_GLOVI	Q7ndf6 gloeobacter

ALIGNMENTS

RESULT 1						
ENP5_HUMAN						
ID	ENP5_HUMAN	STANDARD;	PRT;	428 AA.		
AC	075356;					
DT	16-OCT-2001 (Rel. 40, Created)					
DT	16-OCT-2001 (Rel. 40, Last sequence update)					
DT	15-MAR-2004 (Rel. 43, Last annotation update)					
DE	Ectonucleoside triphosphate diphosphohydrolase 5 precursor					
DE	(EC 3.6.1.6) (NTPDase5) (Nucleoside diphosphatase) (CD39 antigen-like					
DE	4) (ER-JDPase).					
GN	ENTPD5 OR CD39L4.					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUES=Leukemia;					
RX	MEDLINE=98341119; PubMed=9676430;					
RA	Chadwick B.P., Frischauf A.-M.;					
RT	"The CD39-like gene family: Identification of three new human members					
RT	(CD942c, CD942b, and CD942a), their murine homologues, and a member of					
RT	the gene family from Drosophila melanogaster.";					
RL	Genomics 50:357-367(1998).					
CC	FUNCTION: Likely to promote reglycosylation reactions involved in					
CC	glycoproteins folding and quality control in the endoplasmic					
CC	reticulum. Hydrolyzes UDP, GDP AND IDP but not any other					
CC	nucleoside di-, mono- or triphosphates, nor thiamine pyrophosphate					
CC	(By similarity).					
CC	!- CATALYTIC ACTIVITY: A nucleoside diphosphate + H(2)O = a					
CC	nucleotide + phosphate.					
CC	!- COFACTOR: Requires calcium and magnesium.					
CC	!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).					
CC	!- TISSUE SPECIFICITY: Expressed in adult liver, kidney, prostate,					
CC	testis and colon. Much weaker expression in other tissues.					
CC	!- SIMILARITY: Belongs to the GDAL / CD39 NTPase family.					
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -					
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CC	entities requires a license agreement (See http://www.isb-sib.ch/					
CC	or send an email to license@isb-sib.ch).					
CC	EMBL; AF039918; AAC39885.1; -					
CC	Genew; HGNC:3367; ENTPD5.					
DR	MIM; 603162; -					
DR	InterPro; IPR000407; GDAL_CD39_NTPase.					
DR	Pfam; PF01150; GDAL_CD39; 1.					
DR	PROSITE; PS01236; GDAL_CD39_NTPASE; PALSE NEG.					
KW	Hydrolase; Transmembrane; Glycoprotein; Calcium; Magnesium;					
KW	Endoplasmic reticulum; Signal.					
FT	SIGNAL 1 20					
FT	CHAIN 21 428					
FT	ECTONUCLEOSIDE TRIPHOSPHATE					
FT	DIPHOSPHOHYDROLASE 5.					


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DR EMBL; AK002618; BAB22234.1; -.
DR EMBL; BC015247; AAH15247.1; -.
DR MGD; MGI:1321385; Entp05.
DR InterPro; IPR000407; GDA1_CD39_NTPase.
DR Pfam; PF01150; GDA1_CD39; 1.
DR PROSITE; PS01238; GDA1_CD39_NTPase; FALSE NEG.
KW Hydrolase; Transmembrane; Glycoprotein; Calcium; Magnesium;
KW Endoplasmic reticulum; Signal;
FT SIGNAL 1 18
FT CHAIN 19 427
FT CATALYTIC ACTIVITY: A nucleoside diphosphate + H(2)O = a
FT EC: 3.6.1.6 (NTPDase) (Nucleoside diphosphatase)
FT SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
FT TISSUE SPECIFICITY: Expressed in fetal cells and most adult
FT DISEASE: Cph oncogene has transforming capacity and tumorigenic
FT potential.
FT SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
Query Match 88.6%; Score 1994.5; DB 1; Length 427;
Best Local Similarity 88.3%; Pred. No. 1.6e-151;
Matches 377; Conservative 24; Mismatches 25; Indels 1; Gaps 1;
QY 1 MATSWGTFVFMVAVSVCSAVSHRNQOTWTFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSWGAV-FMLIIACVGVSTVFYREQOTWTFEGVFLSSMCPINVSAGTFYGIMFDAGSTGT 59
QY 61 RIHVYTFVQKMPGQLPILGEVDFSVKGLSAFVDQPKQAGTVOGLLEVAKDSIPRSHW 120
DB 60 RIHVYTFVQKMPGQLPILGEVDFSVKGLSAFVDQPKQAGTVOGLLEVAKDSIPRSHW 119
QY 121 KETPVVLKATAGIRLLPEHAKALLFEVKEIFRKSPPFLVPGKSVSMDGSDGILAVTV 180
DB 120 ERTPVVLKATAGIRLLPEHAKALLFEVKEIFRKSPPFLVPGKSVSMDGSDGILAVTV 179
QY 181 NFLTGQHGHRQETVGTGLDGGASTQITFLPQFESKLTQTPRGYLTSPFNFSTPKLYTH 240
DB 180 NFLTGQHGHRQETVGTGLDGGASTQITFLPQFESKLTQTPRGYLTSPFNFSTPKLYTH 239
QY 241 SYLGFGKKAARLATIAGALETEGDTGHTFRSACLPRLWEAEWIFGGVKYQYGGNQEEMGF 300
DB 240 SYLGFGKKAARLATIAGALETEGDTGHTFRSACLPRLWEAEWIFGGVKYQYGGNQEEMGF 299
QY 301 EPCYAEVLVRVKGKLPQEPVQSGSFYAFSYVDRAVDTMDIDYKGGILKVEDFERKAR 360
DB 300 EPCYAEVLVRVKGKLPQEPVQSGSFYAFSYVDRAVDTMDIDYKGGILKVEDFERKAR 359
QY 361 EVCNLENFTSGSPFLCNDLSYITALLKQGGFADSTVLQLTKKVNNIETGVALGATEHL 420
DB 360 EVCNLENFTSGSPFLCNDLSYITALLKQGGFADSTVLQLTKKVNNIETGVALGATEHL 419
QY 421 LQSLIGIS 427
DB 420 LQSLIGIT 426
RESULT 3
ID ENPS MESAU STANDARD; PRT; 469 AA.
AC Q9QYCB; Q9QYCB;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 5 precursor
DE (EC 3.6.1.6) (NTPDase) (Nucleoside diphosphatase) (CD39 antigen-like
DE 4) (ER-UDPase) (Proto-oncogene cph).
GN ENTPD5 OR CD39L4 OR CPH.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]

```

```

RP MEDLINE; 99142925; PubMed-9989819;
RX Velasco J.A., Avila M.A., Notario V.;
RT "The product of the cph oncogene is a truncated, nucleotide-binding
RT protein that enhances cellular survival to stress.";
RL Oncogene 18:689-701(1999).
CC -!- FUNCTION: Likely to promote religyosylation reactions involved in
CC glycoproteins folding and quality control in the endoplasmic
CC reticulum. Hydrolyzes UDP, GDP AND IDP but not any other
CC nucleoside di-, mono- or triphosphates, nor thiamine pyrophosphate
CC (By similarity).
CC -!- CATALYTIC ACTIVITY: A nucleoside diphosphate + H(2)O = a
CC nucleotide + phosphate.
CC -!- COFACTOR: Requires calcium and magnesium (By similarity).
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
CC -!- TISSUE SPECIFICITY: Expressed in fetal cells and most adult
CC tissues.
CC -!- DISEASE: Cph oncogene has transforming capacity and tumorigenic
CC potential.
CC -!- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
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CC or send an email to license@isb-sib.ch).
DR EMBL; AF084568; AAF22931.1; GDA1_CD39_NTPase.
DR EMBL; AF084569; AAF22932.1; -.
DR InterPro; IPR000407; GDA1_CD39_NTPase.
DR Pfam; PF01150; GDA1_CD39; 1.
DR PROSITE; PS01238; GDA1_CD39_NTPase; FALSE NEG.
KW Hydrolase; Transmembrane; Glycoprotein; Calcium; Magnesium;
KW Endoplasmic reticulum; Signal; Proto-oncogene.
FT SIGNAL 1 18
FT CHAIN 19 469
FT CATALYTIC ACTIVITY: A nucleoside diphosphate + H(2)O = a
FT EC: 3.6.1.6 (NTPDase) (Nucleoside diphosphatase)
FT SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
FT TISSUE SPECIFICITY: Expressed in fetal cells and most adult
FT DISEASE: Cph oncogene has transforming capacity and tumorigenic
FT potential.
FT SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
Query Match 85.9%; Score 1933.5; DB 1; Length 469;
Best Local Similarity 86.7%; Pred. No. 1.4e-146;
Matches 364; Conservative 22; Mismatches 31; Indels 3; Gaps 1;
QY 1 MATSWGTFVFMVAVSVCSAVSHRNQOTWTFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATPWGAVFPLMIACAGSTVFIREQOTWTFEGVFLSSMCPANVSASTFYGIMFDAGSTGT 60
QY 61 RIHVYTFVQKMPGQLPILGEVDFSVKGLSAFVDQPKQAGTVOGLLEVAKDSIPRSHW 120
DB 61 RIHVYTFVQKMPGQLPILGEVDFSVKGLSAFVDQPKQAGTVOGLLEVAKDSIPRSHW 120
QY 121 KETPVVLKATAGIRLLPEHAKALLFEVKEIFRKSPPFLVPGKSVSMDGSDGILAVTV 180
DB 121 KETPVVLKATAGIRLLPEHAKALLFEVKEIFRKSPPFLVPGKSVSMDGSDGILAVTV 180
QY 181 NFLTGQHGHRQETVGTGLDGGASTQITFLPQFESKLTQTPRGYLTSPFNFSTPKLYTH 240
DB 181 NFLTGQHGHRQETVGTGLDGGASTQITFLPQFESKLTQTPRGYLTSPFNFSTPKLYTH 240
QY 241 SYLGFGKKAARLATIAGALETEGDTGHTFRSACLPRLWEAEWIFGGVKYQYGGNQEEMGF 300
DB 241 SYLGFGKKAARLATIAGALETEGDTGHTFRSACLPRLWEAEWIFGGVKYQYGGNQEEMGF 300
QY 301 EPCYAEVLVRVKGKLPQEPVQSGSFYAFSYVDRAVDTMDIDYKGGILKVEDFERKAR 360
DB 301 EPCYAEVLVRVKGKLPQEPVQSGSFYAFSYVDRAVDTMDIDYKGGILKVEDFERKAR 360
QY 361 EVCNLENFTSGSPFLCNDLSYITALLKQGGFADSTVLQLTKKVNNIETGVALGATEHL 420

```

Db 361 EVCDNLESTSGSPFLCNDLSVITALLKXGFGADGTLQLTKKNNIETGWPGG---HL 417

RESULT 4 ENP6 HUMAN

AC 075354; Q9UJDI; STANDARD; PRT; 484 AA.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 6 (EC 3.6.1.6)
DE (NTPDase6) (CD39 antigen-like 2).
GN ENTPD6 OR CD39L2.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Keratinocytes;
RX MEDLINE=98341119; PubMed=9676430;
RA Chadwick B.P., Frischauf A.-M.,
RT "The CD39-like gene family: identification of three new human members
RT (CD39L2, CD39L3, and CD39L4), their murine homologues, and a member of
RT the gene family from *Drosophila melanogaster*.";
RL Genomics 50:357-367(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Bead L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grahnam D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.R., Heath P.D., Ho S.C., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Leharalaho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McKay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.P., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromancore A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.E., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RL "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -!- FUNCTION: Might support glycosylation reactions in the Golgi
CC apparatus and, when released from cells, might catalyze the
CC hydrolysis of extracellular nucleotides. Hydrolyzes preferentially
CC nucleoside 5'-diphosphates, nucleoside 5'-triphosphates are
CC hydrolyzed only to a minor extent, there is no hydrolysis of
CC nucleoside 5'-monophosphates. The order of activity with different
CC substrates is GTP > IDP > UDP = CDP >> ADP (By similarity).
CC -!- CATALYTIC ACTIVITY: A nucleoside diphosphate + H(2)O = a
CC nucleotide + phosphate.
CC -!- COFACTOR: Requires calcium and magnesium (By similarity).
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. GOLGI. BUT ALSO
CC OCCURS IN A SOLUBLE EXTRACELLULAR FORM (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: Expressed in most tissues.
CC -!- SIMILARITY: Belongs to the GAI1 / CD39 NTPase family.

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CC -----

DR EMBL; AF039916; AAC39883.1; -;
DR EMBL; AL035252; CAB41571.1; -;
DR GenBank; HGNC:3368; ENTPD6.
DR MIM; 603160; -;
DR InterPro; IPR000407; GDAI_CD39_NTPase.
DR Pfam; PF01150; GDAI_CD39; 1.
DR PROSITE; PS01238; GDAI_CD39_NTPase; FALSE NEG
KW Hydrolase; Transmembrane; Glycoprotein; Calcium; Magnesium;
KW Signal-anchor; Golgi stack.
FT DOVAIN 1 39
FT TRANSXEM 40 60
FT CYTOPLASMIC (POTENTIAL).
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOVAIN 61 484
FT LUMENAL (POTENTIAL).
FT CARBOHYD 220 220
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 284 284
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 138 138
FT V -> L (IN REF. 2).
FT CONFLICT 202 202
FT E -> K (IN REF. 2).
SQ SEQUENCE 484 AA; 53233 MW; 27334B29D8D64C CRC64;

Query Match 44.4%; Score 999; DB 1; Length 484;
Best Local Similarity 52.4%; Pred. No. 4-7e-72;
Matches 204; Conservative 56; Mismatches 123; Indels 6; Gaps 4;

Qy 40 PINVSA---STLYGIMPDAAGTGRTHVYTFVFMGQQLPILGCEVFDVSKVGLSAFVDQ 96
Db 90 FLGTAAADGHEVFGIMFDAGSTGRVHVFOFT-RPPRETPTLTHTETFKAVKGLSAYADD 148
Qy 97 PKGAETVQGLLEKAVKDSIPRSHWKTTPVVLKATAGLRLPEHKAALLPEVKEIPKSP 156
Db 149 VEKSAQIRLELLOVAKQIDIFDFWKATPLVLRKATAGLRLPEHKAALLPEVKEIPKSP 208
Qy 157 FLYPKGSVIMDSDEGILAWTVNFTLQGLHGHROETVGLDLGGASTQITFLPOPEKT 216
Db 209 FLVGDCCVSMNGTDECVSAWITNFTLSLKTGGSSVGMGLGGSGTQIAFLPERVEGT 268
Qy 217 LEOTPRGYLTSFSEWENSTKLYTHSVGLGKLAARLATGALETE-GTDCGHTFSACLP 275
Db 269 LQASPPGLTALRMFNRTYKLYSYLGLGMLARLAILGSGVGPQAKQKELVSPCLSP 328
Qy 276 WLBAEWIFGCVKQYQGNQGEVGFPCYAEVLVRVVRGKLHQPVEVQSGFYAFSYYDR 335
Db 329 SFKGEWEHAEVTVYRVSQKAAAALHSLCAARVSEVLQNRVHRTVEVKGVDYAFSYYDL 388
Qy 336 AVTDMDIVKGGILKVEDPERKARVCONLENTSGSPFLCNDLSVITALLKXGFGAD 395
Db 389 AAGVGLIDAEKGSGLVYGDPEIAAKVVCRTLETQPOSPPSCMDLTVVSLLLQE-FGFP 447
Qy 396 STVLQLTKKVNNIETGWCALGATEFLLQSL 424
Db 448 SKVLKTRKIDNVETSWALGAIHYIDSL 476

RESULT 5
ENP6 RAT
ID ENP6 RAT STANDARD; PRT; 455 AA.
AC Q9ERJ1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 6 (EC 3.6.1.6)
DE (NTPase6) (CD39 antigen-like 2).
GN ENTPD6 OR CD39L2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

SEQUENCE FROM N.A.; SUBCELLULAR LOCATION, AND CHARACTERIZATION.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=20498744; PubMed=11042118;
RA Braun N., Fengler S., Ebeling C., Servos J., Zimmermann H.;
RT "Sequencing, functional expression and characterization of rat
RT NTPase6, a nucleoside diphosphate and novel member of the ecto-
RL Biochem. J. 351:639-647(2000).
CC -!- FUNCTION: Might support glycosylation reactions in the Golgi
CC apparatus and, when released from cells, might catalyze the
CC hydrolysis of extracellular nucleotides. Hydrolyzes preferentially
CC nucleoside 5'-diphosphates, nucleoside 5'-triphosphates are
CC hydrolyzed only to a minor extent, there is no hydrolysis of
CC nucleoside 5'-monophosphates. The order of activity with different
CC substrates is GDP > IDP > UDP = CDP >> ADP.
CC -!- CATALYTIC ACTIVITY: A nucleoside diphosphate + H₂O = a
CC nucleotide + phosphate.
CC -!- COFACTOR: Requires calcium and magnesium.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. GOLGI. BUT ALSO
CC OCCURS IN A SOLUBLE EXTRACELLULAR FORM.
CC -!- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
CC
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CC
CC EMBL: AJ277748; CAC16598.1; -
CC InterPro: IPR000407; GDA1_CD39_NTPase.
CC Pfam: PF01150; GDA1_CD39; 1.
CC PROSITE: PS01238; GDA1_CD39_NTPASE; FALSE NEG.
CC Hydrolase; Transmembrane; Glycoprotein; Calcium; Magnesium;
CC Signal-anchor; Golgi stack.
CC DOMAIN 1 12 CYTOPLASMIC (POTENTIAL).
CC TRANSHEX 13 32 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC (POTENTIAL).
CC FT DOMAIN 33 455 LUMENAL (POTENTIAL).
CC FT CARBOHYD 192 192 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 256 256 N-LINKED (GLCNAC...) (POTENTIAL).
CC SQ SEQUENCE 455 AA; 49899 MW; 19A32E8BAEF0F77B CRC64;
Query Match 43.8%; Score 986; DB 1; Length 455;
Best Local Similarity 54.08; Pred. No. 4.7e-71; Indels 6; Gaps 5;
Matches 204; Conservative 51; Mismatches 117;
49 YGIMFDAGSTGTRIHYVTFQKMPGQLPILGEVFDSPKGLSAFVDQPKQAGETVQGLL 108
74 YGIMFDAGSTGTRIHYVTFQKMPGQLPILGEVFDSPKGLSAFVDQPKQAGETVQGLL 132
109 EVAKDSIPRSHWKTPIVVKATAGRLLPKHAALLPEVKEIF-RKSPFLVPKGSVSI 168
133 NVAKQHIPPYDFWKATPLVVKATAGRLLPKHAALLPEVKEIF-RKSPFLVPKGSVSI 192
169 GSDEGILAWTVNVLFGQLHGHQETVGTLDLGGASTQITFLPQPKTLEOTPRGYLTSF 228
193 GTDEGVSAWITVNLFGSLTSGSSVGMGLDGGSTQITFLPRVETGLQASPGHGLTAL 252
229 EMFNSTYKLTHTSYLGHGLKAARLATLGALETG-ETDGTGTFRACILPRMLEAWIEGGYK 287
253 QMFNFTPLKYSYSLGILGMSARLATLGGVEGPEADDEKELVSPCLSPFRGKWEHART 312
288 YQYGVQGEQGVG-PEPCYAEVLVRVGRKLHPOPEVQSGPYAFSYDYDRAVDTDMDIDYEK 346
313 YRISGQK--AVGLYELCASRVSEVLNKHVHTSEAQHVDFYAFSYDYDRAVDTDMDIDYEK 370
347 GGILKVEDFERKAREVCNLENTSSGPFLLCMDSLYITALLKDGFGFADSTVLQTKYKN 406
371 GGSILVGDFFBIAKYVCKTLETOPSPSPACMDLTVISLLHE-FGPPGDKVLKARKID 429
407 NIETGALGATFHLQLSL 424

DB 430 NVETSWALGAIFHYIDSL 447
RESULT 6
NTPA_PEA
AC NTPA_PEA STANDARD; PRT; 455 AA.
ID P52914;
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nucleoside-triphosphatase (EC 3.6.1.15) (Nucleoside triphosphate
DE phosphohydrolase) (NTPase) (Apyrase).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX NCBI_TaxID=3888;
RX [1]
SEQUENCE FROM N.A.
RC STRAIN=cv. Alaska; TISSUE=Plumule;
RX MEDLINE=96197404; PubMed=8616230;
RA Hsieh H., Tong C.G., Thomas C., Roux S.J.;
RT "Light-modulated abundance of an mRNA encoding a calmodulin-regulated,
RT chromatin-associated NTPase in pea."
RL Plant Mol. Biol. 30:135-147(1996).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=cv. Alaska; TISSUE=Stem;
RA Shibata K., Abe S., Davies E.;
RT "Structure of the coding region and mRNA variants of the apyrase from
RT Pisum sativum."
RL Acta Physiol. Plant. 20:3-13(2001).
CC -!- FUNCTION: Might be involved in RNA transport out of nuclei.
CC -!- CATALYTIC ACTIVITY: NTP + H₂O = NDP + phosphate.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
CC
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CC
CC EMBL: Z32743; CAA83655.1; -
CC EMBL: AB027614; BAB18900.1; -
CC PIR: S65147; S48859.
CC InterPro: IPR000407; GDA1_CD39_NTPase.
CC Pfam: PF01150; GDA1_CD39; 1.
CC PROSITE: PS01238; GDA1_CD39_NTPASE; 1.
CC Hydrolase; Nuclear protein.
CC SQ SEQUENCE 455 AA; 50072 MW; 50FD20023ABC4299 CRC64;
Query Match 21.7%; Score 489; DB 1; Length 455;
Best Local Similarity 33.7%; Pred. No. 2e-31;
Matches 140; Conservative 62; Mismatches 160; Indels 54; Gaps 14;
49 YGIMFDAGSTGTRIHYVTFQKMPGQLPILGEVFDSPKGLSAFVDQPKQAGETVQGL 107
44 YAVVFDAGSTGTRIHYVTFQKMPGQLPILGEVFDSPKGLSAFVDQPKQAGETVQGL 102
108 LEVAKDSIPRSHWKTPIVVKATAGRLLPKHAALLPEVKEIF-RKSPFLVPKGSVSI 166
103 LEQAEVVPDDIQKTPVRLGATAGRLLPKHAALLPEVKEIF-RKSPFLVPKGSVSI 162
167 MDGSEGLAWTVNVLFGQLHGHQETVGTLDLGGASTQITFLPQPKTLEOTPRGYLTSF 222
163 IDGTGEGSVLWTVNVLFGQLHGHQETVGTLDLGGASTQITFLPQPKTLEOTPRGYLTSF 221
223 --GYLTSEFEMNSTYKLTHTSYLGHGLKAARLATLGALETGTFDGTGTFPS--ACLPRLWE 278

(aprase) from potato tubers (Solanum tuberosum).";
 Biochem. Biophys. Res. Commun. 218:916-923(1996).
 [2]
 RN SEQUENCE OF 42-54; 68-95 AND 236-253.
 RC STRAIN-CV, Desires;
 RX MEDLINE=96355615; PubMed=8703025;
 RA Vasconcelos E.G., Ferreira S.T., de Carvalho T.M.U., de Souza W.,
 RA Kettian A.M., Mancilla M.A., Verjovski-Almeida S.,
 RT "Partial purification and immunohistochemical localization of ATP
 RT diphosphohydrolase from Schistosoma mansoni. Immunological cross-
 RT reactivities with potato apyrase and Toxoplasma gondii nucleoside
 RT triphosphate hydrolase";
 RT J. Biol. Chem. 271:22139-22145 (1996).
 RL -!- FUNCTION: Catalyzes the hydrolysis of phosphoanhydride bonds of
 CC nucleoside tri- and di-phosphates.
 CC -!- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
 CC -!- COFACTOR: Calcium.
 CC -!- SUBCELLULAR LOCATION: Membrane-associated (probable).
 CC -!- PTM: The N-terminus is blocked.
 CC -!- SIMILARITY: Belongs to the GDAI / CD39 NTPase family.
 CC
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 CC
 CC EMBL; U58597; AAC02720.1; -;
 DR PIR; J4616; J4616.
 DR InterPro; IPR000407; GDAI_CD39_NTPase.
 DR Pfam; PF01150; GDAI_CD39.1.
 DR PROSITE; PS01238; GDAI_CD39_NTPASE; 1.
 KW Hydrolyase; Transmembrane; Calcium; Signal.
 FT SIGNAL 1 30 POTENTIAL.
 FT CHAIN 31 454 APYRASE.
 FT TRANSMEM 426 446 POTENTIAL.
 FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 454 AA; 50041 MW; 9D98FE431D2A2F52F CRC64;
 SQ SEQUENCE 454 AA; 50041 MW; 9D98FE431D2A2F52F CRC64;
 Query Match 19.8%; Score 446.5; DB 1; Length 454;
 Best Local Similarity 28.8%; Pred. No. 5e-28;
 Matches 131; Conservative 78; Mismatches 177; Indels 69; Gaps 16;
 QY 25 NQQTWFGIFLS-----SMCPINUSA-----STLYGMFDAGSGTGRHVV 65
 DB 3 NQNSHFIFILALFLVPLSLKKNVNAQIPLRHLLSHSEHYAVIFDAGSGSRVVF 62
 QY 66 TFVQXMPGQPLLEG-EVFDVSVKPLSAFVDQPKQAGTVOGLLEVAKDSIPSHWKTTP 124
 DB 63 RFDEKL-GLLPIGNIEYFNATPEGLSSVAEDPKAANSLEPLDGAEGVWPQELQSETP 121
 QY 125 VVLKATAGLRLLPEHKAKALLFEVKEIFR-KSPFLVPKGSVSTMDGSDGILAWVTNVL 183
 DB 122 LELGATAGLRMLKGADEKILQAVNLVKNQSTFHSKQDQVITLDGQEGSYNMAINYL 181
 QY 184 TGLHGRHQRQVTGTLGGAGSTQITFL---PQEKILE-OTPRGYLTSFEMFNSTYKLYT 239
 DB 182 LNLGKDYKSTATIDLGGSQVMAYAI SNEQAKAPQNEDEGPEYVQKHLMSKQNLVY 241
 QY 240 HSYLPGFLKARLATLGALTEGTDGHTFRSACLPLWLEAWTFPGYKIQYGGNQGEVGC 299
 DB 242 HSYLNYQLAGRAEIPKASRNES-----NPCALGECDDGYSGYGVYKVKAPKKG-- 292
 QY 300 FEPYAEVRLAVRG--KLHQPEEVORGSF-----YAFSVYVAVDVTMDI 342
 DB 293 ----SWKCRRLUTHALKINAKCNLEECTFNGVNGGGGQCKNTHASSFPYDIGAQVIV 349
 QY 343 DYE-KGGILKVEDFERKAREVCD-NLENFTS-----GSPFLCMLDSLVTALLKDGFG 392
 DB 350 DTRFPSALAKPIQVNLAAKVAQCTNVADIKSIFPKQDRNIPYLCMDLIYEYTLVVDGFG 409

QY 393 F---ADSTVLQLTQKVVN-IETGWLGNATFHLQ 423
 DB 410 LNPHEKITVHDVQYKYNLVGAAMPGLGCAIDLVS 444
 RESULT 9
 Y4E_CABEL STANDARD; PRT: 485 AA.
 ID Y4E_CABEL
 AC Q18411;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical 54.3 kDa protein C33H5.14 in chromosome IV.
 GN C33H5.14
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OC NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RA Bradshaw H., Stellyes L.; to the EMBL/GenBank/DBJ databases.
 RL Submitted (DEC-1995) to the GDAI / CD39 NTPase family.
 CC -!- SIMILARITY: Belongs to the GDAI / CD39 NTPase family.
 CC
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 CC
 CC EMBL; U41007; AAA82272.1; -;
 DR PIR; T34147; T34147.
 DR WormPep; C33H5.14; CE04157.
 DR InterPro; IPR000407; GDAI_CD39_NTPase.
 DR Pfam; PF01150; GDAI_CD39.1.
 DR PROSITE; PS01238; GDAI_CD39_NTPASE; 1.
 KW Hypothetical protein; Transmembrane; Hydrolase.
 FT TRANSMEM 439 459 POTENTIAL.
 FT SEQUENCE 485 AA; 54309 MW; DE64DIADC20F581E CRC64;
 Query Match 17.2%; Score 387.5; DB 1; Length 485;
 Best Local Similarity 27.7%; Pred. No. 2.8e-23;
 Matches 120; Conservative 84; Mismatches 152; Indels 77; Gaps 18;
 QY 49 YGIMFDAGSGTGRHVVTFVQKMPGQPLLEGVFDV-----VKPLSAFVDQPKQAG 102
 DB 25 YGVICDAGSGTGRHVVTFVQKMPGQPLLEGVFDV-----VKPLSAFVDQPKQAG 83
 QY 103 TVQGLLEVAKDSIPSHWKTTPVVLKATAGLRLLPEHKAKALLFEVKEIFRKSPPFL-VPK 161
 DB 84 YLTPLLRPAEEHIPYEQLGSETDLLIFATAGMELLPAAQKDAIKNLQNLKSVTLRVSD 143
 QY 162 GSVISMDGSDGILAWVTNVLTLGHLGRHQRQVTGTLGGAGSTQITELPQPEK----- 215
 DB 144 SNIRIIDGAWEGHYKNIAYNVTILGFTDKENDSKVMIDMGASVQIAFIAEKESYNGG 203
 QY 216 TLEQTPRGYLTSEFMFNSTYKLYTHSYLGFGLKAAARLATLGALTEGTDGHTFRSACLPR 275
 DB 204 NYVEINLGSIEINEDYK--YKIVSTFLGYGANEGLKKYENSILVKSGNS---NDCSPR 257
 QY 276 WLEAEWIFGCVKQYGGNQGEVGEVGPYAEVLRVVRGKLHQPE----- 319
 DB 258 GLNR--LIG-----EFTVNGTGE--MDVCLAQVSSLI-GDKAFSPCNPTCFRLNVIAPSV 308
 QY 320 EYQGSFVAFS--YYIDRAVDTDMDIYKGGILKVEDFERKAREVC-----DNLNFTSGSP 374
 DB 309 NLSTVQLYGFSEYWTTS-----NFGSGEYHYQKFTDEVKCYCKQKWNIDQDGFRNE 362
 QY 375 F-----LMDLSYITALLKDGFGFADST--VLQLTQKVVN-IETGWLGNATFHLQ 416

Db 363 FPNADIERLGTNCFKAAWTSVLHDSFN-VDKTKHLFQSVLKIAGEEMQALGMLYHSK 421
Qy 417 --TFPHLLQSLGIS 427
Db 422 DLKFNLEQLEVA 434
RESULT 10
YBU4_CABEL STANDARD; PRT; 552 AA.
AC Q21815;
DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hydrothermal protein R0784.4 in chromosome X.
GN R0784.4
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
ON NCBI_TaxID=6239;
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Miller N.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN REVISIONS.
RA Waterston R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
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CC
CC EMBL; U39652; AAA80403.2; -
DR WormPep; R0784.4; CE28748.
DR InterPro; IPR000407; GDA1_CD39_NTPase.
DR Pfam; PF01150; GDA1_CD39_1.
DR PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
KW Hypothetical protein; Transmembrane; Hydrolase.
FT TRANSMEM 7 27
FT TRANSNEM 490 510
FT SEQUENCE 552 AA; 62510 MW; B5DC32C858AE4D94 CRC64;
Query March 17.18; Score 385; DB 1; Length 552;
Best Local Similarity 28.68; Pred. No. 5.2e-23;
Matches 126; Conservative 69; Mismatches 160; Indels 86; Gaps 20;
Qy 49 YGINEDAGSTGTRHIVYTFVQKMPGQLPILGEVFDG-----VKPGLSAFVDPQKQAE 102
Db 44 YGVICDAGSTGTRLFVYVNWISTSDSELIQIEPVYDKNKPVWKKISPLGSLTFGKPAQAE 103
Qy 103 TVQGLLVAKDSIPRSHKKTTPVVLKATAGLLPEHKAKALLPEVKEIFRKSPEL---- 158
Db 104 YLRPLMEALRHPIEERKRPYPYFIPATAGNRLIPDEQKEAVL---KLNRLKLPKITSQ 160
Qy 159 VPKGSVIMDGSDEGILAVTNFNLTCQLH-----GH-RQETVGTLDLGCAS 205
Db 161 VLKEHRIIEGKMEGIYSWIAVNVYALGFENKNTATLDFPGTSPAARQKTVGMIDMGASA 220
Qy 206 QITP-LIQPEK-----TLQRTGRVLTSEFNPSTYKLYTHSYLGF-----GLKAAALATLG 256
Db 221 QIAFELPDTDSFSSINVENIMLGCREDSDLFK--YKLFVTFTFLGYGVNBIKYEYHMLLS 278
Qy 257 ALETGTDGHTFRACLPRLMLEAEWIFGVKQYQXGN--OEG-----E 297
Db 279 XLKQD--NGTVIQDDCPNLNLT-----VTLENGENFVRRTGNTWCNEVKKLNP 331

Qy 298 VGFPPCAEVLVRVVRGKLHOPE-EVQRGSFYAFSVYVYDRAVDTDMDIDYKGGILKVEDFE 356
Db 332 SSSVEVCAEAAKCYFGAVPAPSPILSNIEVMYGPSEYVYSHDV---LGLGGQYDAENIA 387
Qy 357 RKAREVCD-----NLENFTSGSP-----FLCMDLSYITALLKQDGFADST--VLQ 400
Db 388 KKTQYCSKRWSTTQAEBSKQLYPRADEERLRTQFKSAWTSVLHDFGS-VDKTHNFKQ 446
Qy 401 LTKKVNNTETGMALGA-TFHL 420
Db 447 SVSTIAGQEVQVQALGMNIYEM 467
RESULT 11
ID ENP1_CHICK STANDARD; PRT; 493 AA.
AC O93295;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE (NTPDase1) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid cell
DE activation antigen) (Ecto-apyrase) (CD39 antigen).
GN ENTPD1 OR CD39.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-21 AND 150-156.
RC TISSUE=Oviduct;
RX MEDLINE=98298108; PubMed=9632655;
RA Nagy A.K., Knowles A.F., Nagami G.T.;
RT "Molecular cloning of the chicken oviduct ecto-ATP-
RT diphosphohydrolase."
RL J. Biol. Chem. 273:16043-16049 (1998).
RN [2]
RP SEQUENCE OF 1-17.
RC TISSUE=Stomach;
RX MEDLINE=97442428; PubMed=9295305;
RA Lewis-Carl S., Kirley T.L.;
RT "Immunolocalization of the ecto-ATPase and ecto-apyrase in chicken
RT gizzard and stomach. Purification and N-terminal sequence of the
RT stomach ecto-apyrase."
RL J. Biol. Chem. 272:23645-23652 (1997).
CC -1- FUNCTION: In the nervous system, could hydrolyze ATP and other
CC nucleotides to regulate purinergic neurotransmission. Could also
CC be implicated in the prevention of platelet aggregation.
CC Hydrolyzes ATP and ADP equally well (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
CC -1- COFACTOR: Requires calcium and magnesium (By similarity).
CC -1- SUBUNIT: Homodimer; disulfide-linked (Probable).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- PTM: N-glycosylated.
CC -1- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
CC
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CC
CC EMBL; AF041355; AAC26491.1; -
DR InterPro; IPR000407; GDA1_CD39_NTPase.
DR Pfam; PF01150; GDA1_CD39_1.
DR PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
KW Hydrolase; Transmembrane; Antigen; Glycoprotein; Calcium; Magnesium.
FT DOMAIN 1 7
FT TRANSNEM 8 28
FT TRANSMEM 1 28

FT DOMAIN 29 463 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 464 486 POTENTIAL.
FT DOMAIN 487 493 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 65 65 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 73 73 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 133 133 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 223 223 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 267 267 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 324 324 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 330 330 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 361 361 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 372 372 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 16 16 C -> W (IN REF. 2).
FT CONFLICT 21 21 I -> G (IN REF. 1); AA SEQUENCE).
SQ SEQUENCE 493 AA; 54034 MW; F14FF4C3AA2F3603 CRC64;

Query Match 17.0%; Score 383; DB 1; Length 493;
Best Local Similarity 27.3%; Pred. No. 6,4e-230;
Matches 131; Conservative 66; Mismatches 170; Indels 112; Gaps 18;

QY 11 MLWVSCVCAVSHRNQOTWFGIFLSSMCPINVSASTLYGIMFDAGSTGTRIHVYTF-VQ 69
DB 11 LITATCVFSIIALLSANDVKDFL-----PPCTKGLVFDAGSTHATLYVYQMPAD 62

QY 70 KMPGQPILEGVDFDSVKGLSAFVDPQKQASTVQGLLEVAKDSIPRSHWKKTPVVLKA 129
DB 63 KENGTVGSQVESCCTVNGSGISSYADDPAGASLXPCLDKAMAVIPVQOMQTPPYLGA 122

QY 130 TAGRLRLPEH---KAKALLPEVKEIPKSPFLPKGSVIMDSGDEGILLAVTNVSLTQ 186
DB 123 TAGRLLRQNSTKARQVFAEVSXAIRBP--VDPRGAQLTGNESGFGNTVNVLLT 180

QY 187 L-----HGHRETQVGLDGGASTQITPLPQFEKTLQTPRGYLTSPFNFSTYK 236
DB 181 LKFSFAGKWEHPQNTVEVLGALDGGASTQITPQGV--TIEDKNTSVL--FRLYGTNTS 236

QY 237 LYTHSVLGLCLXARLATIGALTECTDGHFESACLPRLWLEAEWIFPGVKYQYGNQB- 295
DB 237 LYTHSVLGLCGIQASKRLMAALHQDSYVQNTSHPCYPK-----GYRI 280

QY 296 ---GEVGFPEFCY-----AEVLRYVR-----GKLLHQ 317
DB 281 ITIAEIVDPVCVTPSMSPAILITVTGNGNPAACPTAILKLFNLTCGANRTCGFDGVYQ 340

QY 318 PEEVQGSFVAFS-YYIDRA-----VDTMDYD-EKGGILKYEDPERKAREVC 363
DB 341 PP--VRGQFFAFAGFYTFESFLNLTCQQLSHVNATVDFPCNKMSSELVETFPQNK---- 394

QY 364 DNLENSTGSPFLCMDLSYITALLKDGFGFADST--VLQLTKKVNNIETGWLGAFTHL 420
DB 395 EHLHYT-----CVVGLITLLVDGYKFDERTNSNIHFSQKAGNADIGTLGFWMLNL 446

RESULT 12
YND1 YEAST
ID YND1 YEAST STANDARD; PRT; 630 AA.
AC P4009;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Golgi apyrase (EC 3.6.1.5) (ATP-diphosphatase) (Adenosine
DE diphosphatase) (ADPase) (ATP-diphosphohydrolase) (Golgi nucleoside
DE diphosphatase).
GN YND1 OR YER005M.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.

RC STRAIN=S288c;
RX MEDLINE=99340091; PubMed=10409709;
RA Gao X.D., Kalgorodov V., Jigami Y.;
RT "YND1, a homologue of GDA1, encodes membrane-bound apyrase required
RL for Golgi N- and O-glycosylation in Saccharomyces cerevisiae.";
RN J. Biol. Chem. 274:21450-21456(1999).
RP [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RX MEDLINE=97313264; PubMed=9169868;
RA Dietrich P.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E.,
RA Cherray J.M., Aviles E., Berno A., Brennan T., Carpenter J., Chen E.,
RA Hunick-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari D., Lew H.,
RA Lin D., Moseadale D., Nakahara K., Namath A., Norgren R., Oefner P.,
RA Oh C., Petel P.X., Roberts D., Sehl P., Schramm S., Shogren T.,
RA Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;
RL "The nucleotide sequence of Saccharomyces cerevisiae chromosome V.";
RT Nature 387:78-81(1997).
CC -!- FUNCTION: Catalyzes the hydrolysis of phosphoanhydride bonds of
CC nucleoside tri- and di-phosphates. Has equal high activity toward
CC ADP/ATP, GTP/GDP, and UDP/UTP and approximately 50% less toward
CC CDP/CTP and thiamine pyrophosphate. Has no activity toward GMP.
CC Required for Golgi glycosylation and cell wall integrity.
CC -!- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
CC -!- PATHWAY: Glycosylation.
CC -!- SUBCELLULAR LOCATION: Golgi; membrane-bound.
CC -!- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
CC
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CC
CC EMBL; AF203695; AAF17573.1; --
CC EMBL; U18778; AAB64538.1; --
CC PIR; S50463; S50463.
CC GeneOnline; 139085; --
CC SGD; S0000807; YND1.
CC GO; GO:0017110; F:nucleoside diphosphatase activity; IDA.
CC GO; GO:0006486; P:protein amino acid glycosylation; IMP.
CC InterPro; IPR000407; GDA1_CD39_NTPase.
CC Pfam; PF01150; GDA1_CD39_1.
CC PROSITE; PS01238; GDA1_CD39_NTPase; 1.
KW Hydrolase; Transmembrane; Golgi stack.
FT DOMAIN 1 500 LUMENAL (POTENTIAL).
FT TRANSMEM 501 517 POTENTIAL.
FT DOMAIN 518 630 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 630 AA; 71851 MW; 02F8D24A78212544 CRC64;

Query Match 16.5%; Score 372; DB 1; Length 630;
Best Local Similarity 26.2%; Pred. No. 6.8e-22;
Matches 117; Conservative 73; Mismatches 165; Indels 92; Gaps 17;

QY 49 YGIMFDAGSTGTRIHVYTF-----VQKMPQQLPICE---VFDSVVKPLSA 92
DB 10 FGIVIDAGSSGRHVFVKWQDTESSLHATNQDSQSLQSVPHIQEKDWTFLKPLGLSS 68

QY 93 PVDQPKQCAET-VQGLLEVAKDSIPRSHWKKTPVVLKATAGRLPEHKAALFEV-KE 150
DB 69 FEKKPQDQAYSHIKPLLDFAKNIPESHWSGCPFIQATAGRLLPDIQISLDGLCQG 128

QY 151 IFRKSPFLVP--KGSVSIMDSGDEGILLAVTNVFLTQGLHGRQD-----TVGTLDLGA 203
DB 129 LKHPAEFLVEDCSAQIQVIDGETEGLYGLGLNLYGHFNFDYNPEVSHFTFGFMDGGA 188

QY 204 STQITFLPQPEKTL-----QTPRGYLTSPFNFSTYKLYTHSVLGFGLKARL 252
DB 189 STQIAFAPHSQGEIARHDDIATIFLRVNGDLQKQDFVST-----WLGFGANQARR 241

Query Match 16.5%; Score 372; DB 1; Length 630;
Best Local Similarity 26.2%; Pred. No. 6.8e-22;
Matches 117; Conservative 73; Mismatches 165; Indels 92; Gaps 17;


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QY 253 ATLGAL-----ETEGTGTGHTFRSACLPRWLAEWIFGVGVKYQYGGNQEVEGPE 301
DB 242 RYLAQLINTLPENTNDYENDDFSRNLNDFPCMRGSSSTDFEFDXTIFPHIAGSNYEQCTK 301
QY 302 PCTAEVLR-----VVRGKLHQPZ-EVORGFSFYAFSYTIDRAVTDMDYKGGILKV 352
DB 302 SIYPLLLKNPCDDPECLFNGVAPRIDFANDKFIGTSETWYANDV-----FKLGSEYNF 357
QY 353 EDPERKAREVCN-----LENFTSG-----SPL-----CMLSVITALLKXGFGFA---- 394
DB 358 DKFSKSRREPCNSNWTOLANSKGVNSIPENFLKDACFKGNWLVNLIEHGEFOMPRIDV 417
QY 395 -----DSTVLQLTKVNNIETGWALG 415
DB 418 DAENVNDRPLFQSVKVEREELSWTLG 444

RESULT 13
ENPI_MOUSE STANDARD; PRT; 510 AA.
ID ENPI_MOUSE
AC P55772;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE (NTPDase1) Ecto-ATP diphosphohydrolase (ATPDase) (lymphoid cell
DE activation antigen) (ecto-apyrase) (CD39 antigen).
GN ENTPD1 OR CD39.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95015846; PubMed=7930580;
RA Maliszewski C.R., Deleseppe G.J.T., Schoenborn M.A., Arnitage R.J.,
RA Fanslow W.C., Nakajima T., Baker E., Sutherland G.R., Poindexter K.,
RA Birks C., Albert A., Friend D., Gimpel S.D., Gayle R.B. III;
RT "The CD39 lymphoid cell activation antigen. Molecular cloning and
RT structural characterization."
RL J. Immunol. 153:3574-3583(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=98399871; PubMed=9730622;
RA Schoenborn M.A., Jenkins N.A., Copeland N.G., Gilbert D.J.,
RA Gayle R.B. III, Maliszewski C.R.;
RT "Gene structure and chromosome location of mouse Cd39 coding for an
RT ecto-apyrase."
RL Cytogenet. Cell Genet. 81:287-289(1998).
CC -1- FUNCTION: In the nervous system, could hydrolyze ATP and other
CC nucleotides to regulate purinergic neurotransmission. Could also
CC be implicated in the prevention of platelet aggregation.
CC Hydrolyzes ATP and ADP equally well.
CC -1- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
CC -1- COFACTOR: Requires calcium and magnesium (By similarity).
CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
CC
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CC
CC -----
CC EMBL; AF037366; AAB92259.1; --
CC EMBL; AF041818; AAC83203.1; --
CC EMBL; AF041812; AAC83203.1; JOINED.
CC EMBL; AF041813; AAC83203.1; JOINED.
CC EMBL; AF041814; AAC83203.1; JOINED.

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DR EMBL; AF041815; AAC83203.1; JOINED.
DR EMBL; AF041816; AAC83203.1; JOINED.
DR EMBL; AF041817; AAC83203.1; JOINED.
DR MGD; MGI:102805; Entpdl
DR GO; GO:0003605; Cerebral lamina; IDA.
DR GO; GO:0004050; P-ATPase activity; IDA.
DR GO; GO:0006200; P-ATP catabolism; IDA.
DR GO; GO:0007186; P-G-protein coupled receptor protein signalin. .; IDA.
DR GO; GO:0030168; P-platelet activation; IDA.
DR GO; GO:0009181; P-purine ribonucleoside diphosphate catabolism; IDA.
DR InterPro: IPR000407; GDA1_CD39_NTPase.
DR Pfam; PF01150; GDA1_CD39_1.
DR PROSITE; PS01238; GDA1_CD39_NTPase; 1.
KW Hydrolase; Transmembrane; Antigen; Glycoprotein; Calcium; Magnesium.
FT DOMAIN 1 16 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 17 37 POTENTIAL.
FT DOMAIN 38 478 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 479 499 POTENTIAL.
FT DOMAIN 500 510 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 73 73 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 226 226 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 291 291 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 333 333 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 428 428 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 510 AA; 57205 MW; 8E6A6113D2E13930 CRC64;

Query Match 16.4%; Score 370; DB 1; Length 510;
Best Local Similarity 27.1%; Pred. No. 7.3e-22;
Matches 121; Conservative 71; Mismatches 173; Indels 82; Gaps 19;

QY 32 GTFLLSMCPINVSASTLYGIMPDAGSTGRIHVYTFVOKMPQQLPILEGEVDSVK-PGL 90
DB 36 GUTQKPLPENVK-----YQIVLDAGSSHTNLYIKNPAEKENDTGVVQQLBECQVKGPI 91
QY 91 SAFVDQPKQGAETVQGLLEVAKDSIPRSHWKTTPVVLKATAGLRLL---PEHAKALLPE 147
DB 92 SKVAQKTDEIGAYLAECMELSTELIPTSKHQTPVYLGATAGMLLRMESEQSADEVLA 151
QY 148 YKEIFRKPPLVPKGSVIMDGSDEGILAWTVNLTGOL-----HGRQETVG 196
DB 152 VSTSLKSYFF--DFQAKIITQGBEGAYGWIITNLGLRFTQEQSWLSLSDSQKETFG 209
QY 197 TLDLAGASTQITFLPQFETKLEOTPRGYLTSEMFNSTYKLYTHSYLGFGLKAARLATIG 256
DB 210 ALDLAGASTQITFVPQ-NSTIE-SFENSL-QFLYGEDYTVYTHSFCLYCKQDALWQKL- 265
QY 257 ALETSGTGTHTFRSACL-----PRWLAEWIFGVGVKYQYGGNQEVE 298
DB 266 AKDIQVSSGGVILKPCFNPGEKVVNSELVGTCTKFEKGLPFDQPRIQTGD----- 320
QY 299 GPEPCVAEVLRVVRGKLHQPZ-----VORGFSFYAFSYTIDRAVTDMDY---- 344
DB 321 -VEQCHQSILELFNNS-HCPYSQCAFNGVFLPPLHGSFGAFSAFY-----PVMDFEKV 372
QY 345 EKGKILKVEDFERKAREVCD-NLENFTSGSPL-----CMLSVITALLKXGFGFA 395
DB 373 AKNSVISQEKMTETITNFCSSKSWETKTSYPSVKEKYLSEYCFSGAYILSLQ-GYNFTD 431
QY 396 STVLQI--TKKVNNIETGWALGATPHL 420
DB 432 SSWEQLHFMGKIDSNAGTLYMLNL 458

RESULT 14
ENPI_BOVIN STANDARD; PRT; 513 AA.
ID ENPI_BOVIN
AC O18956;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE (NTPDase1) (Ecto-ATP diphosphohydrolase) (ATPDase) (lymphoid cell

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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong E.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong E.,
RA Brownstein M.J., Udell T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Yadan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
RX MEDLINE=20317099; PubMed=10858452;
RA Biederick A., Kusan C., Kunz J., Bissasser H.-P.;
RT "First asparase splice variants have different enzymatic properties.";
RL J. Biol. Chem. 275:19018-19024(2000).
CC -!- FUNCTION: Hydrolyzes preferentially nucleoside 5'-diphosphates,
CC nucleoside 5'-triphosphates are hydrolyzed only to a minor extent
CC (by similarity).
CC -!- CATALYTIC ACTIVITY: A nucleoside diphosphate + H(2)O = a
CC nucleotide + phosphate.
CC -!- COFACTOR: Requires calcium and magnesium.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC Localizes in the Golgi and autophagic vacuoles/lysosomes (By
CC similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=LALP70;
CC IsoId=Q9DBT4-1; Sequence=displayed;
CC Name=2; Synonyms=LALP70V;
CC IsoId=Q9DBT4-2; Sequence=VSP_003615;
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- SIMILARITY: Belongs to the GDAI / CD39 NTPase family.
CC -----
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CC -----
DR EMBL; AK004761; BAB23542.1; -;
DR EMBL; BC006924; AAR06924.1; -;
DR EMBL; BC043134; AAR43134.1; -;
DR MGD; MGI:1914714; Lysal1.
DR InterPro; IPR000407; GDAI_CD39_NTPase.
DR Pfam; PF01150; GDAI_CD39_1.
DR PROSITE; PS01238; GDAI_CD39_NTPase.
KW Hydrolase; Transmembrane; Glycoprotein; Calcium; Magnesium;
KW Alternative splicing; Golgi stack; Lysosome.
FT DOMAIN 1 33 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 34 54 POTENTIAL.
FT DOMAIN 55 559 LUMENAL (POTENTIAL).
FT TRANSMEM 560 580 POTENTIAL.
FT DOMAIN 581 613 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 407 407 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPIC 287 294 Missing (in isoform 2).
FT FTID=VSP_003615.
SQ SEQUENCE 613 AA; 69745 MW; DES28F512ABEF52P CRC64;

Query Match 16.0%; Score 360.5; DB 1; Length 613;
Best Local Similarity 24.4%; Pred. No. 5.4e-21;

	Matches	127;	Conservative	77;	Mismatches	185;	Indels	131;	Gaps	21;
QY	11	MLVSCVCSAVS	-----ERNQOTWPE	-----GIFLSSMCPINV	-----SASTLYGIMF	53				
DB	34	IVVISILAAAVSLLYF	SVVILIRSKYGLSKDKK	QFQRLARVTDVBAT	TNNPSVNYIVV	93				
QY	54	DAGSTGTIRHVYTFV	QKMPGQLPILS	-----GEVFD	SVKPGLSAFVDQPKQGAETV	104				
DB	94	DCGSSGSRIFVYCW	PHNGNPHDDLDIRQ	MRDKNRKPVVMKIK	PGISEFATSPKVSVDYI	153				
QY	105	QGLLVAKDSIPRSHW	KKTIVVVKATAGRL	LLPEHKALLFEVKEI	FRKSP-----FLVP	160				
DB	154	SPLLSFAAHVPRAK	KETPLYLITAGMRV	LPESQKAIL-----BDLLT	DPVHYDFLFS	210				
QY	161	KGSVIMDGSDEGIL	AWTVNFLTQGLGH	-----RORTVGT	197					
DB	211	DSHARVIGKQGGV	AMTGINFVLGRFE	-----HIEED	EAUVENNIPOSESE	269				
QY	198	LDLGGASTOITF	LPQ-----FEKTL	EQTPRGYLTSEFEM	-----FNSTYKLYTHSYLQFG	246				
DB	270	LDMGGVSTQIAYE	VPQTVSVFASSQ	QOEBAKLLAEFNLG	CDVHQTEHYVRYVYVATFLQFG	329				
QY	247	LKAARSLA	-----TLGALET	SGTDGHTFRSACL	PRWLAEAMIFGGVKYQYGN	293				
DB	330	GNAARQRYEDRL	FASTVQKRNLLG	KQGLTPDAPLLD	PLDIDKDE-----LQNGQ	382				
QY	294	Q-----EGEVGF	PCYAEVLRVVRGK	LHQ-----PEEVQ	SGSPYAFSYXDRAVDT	339				
DB	383	TLYLQGTGDFDL	C-RETLQPF	PANKTNETQTSING	VYQPPINFQNESEFYGFSEFYCTEDV	441				
QY	340	DMIDYEKGILK	VEDFERKARECDN	-----LENPTSG	-----SPFLCMDLSYIT	384				
DB	442	-----LRMG	GDVNAARFTQA	KDKYCATKWSIL	RERPDRLGYASHADLHRLKYQCFKSAMWF	497				
QY	385	ALLKDGFGFADS	-----TVLQ	LTKVNNIETG	WALGATFH	419				
DB	498	EVPHKGFSPV	TYKMLKALQVYDK	-----EVQW	TGLALY	533				

Search completed: July 1, 2004, 13:47:09
Job time : 12 secs

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OM protein - protein search, using sw model

Run on: July 1, 2004, 13:43:06 ; Search time 38.5 Seconds
(without alignments)
3507.579 Million cell updates/sec

Title: US-10-091-085-3
Perfect score: 2250
Sequence: 1 MATSGTTFPMLVWSCVCSA.....ETGWAIGATFLLQSLGISH 428

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2236	99.4	428	Q96RX0	Q96rx0 homo sapien
2	2104	93.5	407	Q8WUB3	Q8wub3 homo sapien
3	1990.5	88.5	427	Q8CD29	Q8cd29 mus musculus
4	1984.5	88.2	427	Q8BR23	Q8br23 mus musculus
5	996	44.3	483	Q8TAS7	Q8tas7 homo sapien
6	996	44.3	484	Q725B5	Q725b5 homo sapien
7	996	44.3	503	Q8N3H3	Q8n3h3 homo sapien
8	696.5	31.0	461	O76268	O76268 drosophila
9	696.5	31.0	464	Q9VQI8	Q9vqi8 drosophila
10	616.5	27.4	479	Q9XU84	Q9xu84 caenorhabdi
11	593	26.4	278	Q8CH23	Q8ch23 mus musculus
12	538.5	23.9	556	Q9UT35	Q9ut35 schizosacch
13	518.5	23.0	455	Q84UE0	Q84ue0 medicago tr
14	518.5	23.0	489	Q8H7L6	Q8h7l6 oryza sativ
15	515.5	22.9	599	Q8TGH6	Q8tgh6 candida alb
16	511	22.7	522	Q9HEM6	Q9hem6 kluyveromy

17	507.5	22.6	455	10	Q9SPM6	Q9spm6 medicago sa
18	501.5	22.4	467	10	Q9SPM7	Q9spm7 dolichos bi
19	498	22.1	462	10	Q9XFC9	Q9xfc9 dolichos bi
20	498	22.1	466	10	Q84UE2	Q84ue2 medicago tr
21	492	21.9	467	10	Q84UD8	Q84ud8 medicago tr
22	491.5	21.8	456	10	Q9SPM8	Q9spm8 lotus japon
23	491	21.8	455	10	Q84L88	Q84l88 glycine max
24	489	21.7	455	10	Q9PEA6	Q9pea6 pisum sativ
25	489	21.7	472	10	Q8L704	Q8l704 arabidopsis
26	488	21.7	463	10	Q9FVC3	Q9fvc3 glycine soj
27	488	21.7	472	10	Q9SPM5	Q9spm5 arabidopsis
28	486	21.6	455	10	Q8GTB1	Q8gtb1 pisum sativ
29	485	21.6	472	10	Q9M7B3	Q9m7b3 arabidopsis
30	484	21.5	471	10	Q9SQG2	Q9sqg2 arabidopsis
31	481	21.4	447	10	Q9SIV4	Q9siv4 pisum sativ
32	480.5	21.4	467	10	Q84UE1	Q84ue1 medicago tr
33	476.5	21.2	455	10	Q84UD9	Q84ud9 medicago tr
34	475	21.1	468	10	Q9FVC2	Q9fvc2 glycine soj
35	473	21.0	467	10	Q8RTV6	Q8rtv6 pisum sativ
36	472	21.0	407	10	Q9AVN8	Q9avn8 pisum sativ
37	472	21.0	455	10	Q8RVU0	Q8rvu0 pisum sativ
38	465	20.7	447	10	Q9FUI1	Q9fui1 pisum sativ
39	464.5	20.6	558	3	Q8TGS8	Q8tgs8 aspergillus
40	462	20.5	466	10	Q9AUI5	Q9aul5 medicago tr
41	454	20.2	454	10	Q84UE3	Q84ue3 medicago tr
42	449	20.0	455	10	Q8RTV9	Q8rtv9 pisum sativ
43	443	19.7	473	10	Q8RTV8	Q8rtv8 pisum sativ
44	436.5	19.4	556	3	Q9C2M0	Q9c2m0 neurospora
45	435.5	19.4	271	5	Q8IPZ6	Q8ipz6 drosophila

ALIGNMENTS

RESULT 1

Q96RX0 PRELIMINARY: PRT: 428 AA.

AC Q96RX0;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Pcp proto-oncogene protein.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.

RX MSBLINE=20173601; PubMed=10708485;

RA Recio J.A., Zambrano N., Pena, Ld, Reig J.A., Rhoads A., Rouzaut A.,

RA Ncarlo V.;

RT "The human PCP proto-oncogene: cDNA identification, primary

RT structure, chromosomal mapping, and expression in normal and tumor

RT cells.";

RL Mol. Carcinog. 27:229-236(2000).

DR EMBL: AF136572; AAR82950.1; "

DR InterPro: IPR000407; GDAI_CD39_NTPase.

DR Pfam: PF01150; GDA_CD39; 1.

SQ SEQUENCE 428 AA; 47431 MW; P2C4F7DE650A44F6 CRC64;

Query Match 99.4%; Score 2236; DB 4; Length 428;

Best Local Similarity 99.5%; Pred. No. 6.4e-184;

Matches 426; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MATSGTTFPMLVWSCVCSA...SHRNQQTWFGIGFLSSMCPINVSASTLYGIMFDAGSTGT 60

Db 1 MATSGTTFPMLVWSCVCSA...SHRNQQTWFGIGFLSSMCPINVSASTLYGIMFDAGSTGT 60

Qy 61 RIHYVTFVQKMPGOLPILEGVFDSPVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120

Db 61 RIHYVTFVQKMPGOLPILEGVFDSPVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120

Qy 121 KKTDPVLKATAGLRLPEHKAKALLFEVKEIFRSPFLVPGKSVSIMDGSDEGLAWTVV 180

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Db 121 KKTPTVVLKATAGLRLLPEHKAALLFEVKEIFRKSFFLPVPGSVSMDGSDGILAWTV 180
Qy 181 NFLTQGLHGRQRTVGTGLDGGASTQITFLPQPEKTELEQTPRGYLTSEFNFNSTYKLYTH 240
Db 181 NFLTQGLHGRQRTVGTGLDGGASTQITFLPQPEKTELEQTPRGYLTSEFNFNSTYKLYTH 240
Qy 241 SYLGFGLKAARLATLGALETEGTDGHTFRSACLPRWLEAEWIFGGVKYQYGGNQGEVGF 300
Db 241 SYLGFGLKAARLATLGALETEGTDGHTFRSACLPRWLEAEWIFGGVKYQYGGNQGEVGF 300
Qy 301 EPCYAEVLVRVGRKHLQPEEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
Db 301 EPCYAEVLVRVGRKHLQPEEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
Qy 361 EVCDNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQ 400
Db 361 EVCDNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQ 400
Qy 421 LOSIGISH 428
Db 421 LOSIGISH 428

RESULT 2
Q8WUB3 PRELIMINARY; PRT; 407 AA.
AC Q8WUB3;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Similar to ectonucleoside triphosphate diphosphohydrolase 5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020966; AAH20966.1; -.
DR GO; GO:0016787; P:hydrolase activity; IEA.
DR InterPro; IPR000407; GDAL_CD39_NTPase.
DR Pfam; PF01150; GDAL_CD39; 1.
KW Hydrolase.
SQ SEQUENCE 407 AA; 45336 MW; D92A5F7DC9EC9E5B CRC64;

Query Match 93.5%; Score 2104; DB 4; Length 407;
Best Local Similarity 100.0%; Pred. No. 1.4e-172;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATSWGTVFFMLVVCVCSAVSHRNQQTWPEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
Db 1 MATSWGTVFFMLVVCVCSAVSHRNQQTWPEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
Qy 61 RIHVYTFVQKMPGQPLILEGEVDSVPGLSAFVDQPKQAEIVQGLLEVAKDSIPRSHW 120
Db 61 RIHVYTFVQKMPGQPLILEGEVDSVPGLSAFVDQPKQAEIVQGLLEVAKDSIPRSHW 120
Qy 121 KKTPTVVLKATAGLRLLPEHKAALLFEVKEIFRKSFFLPVPGSVSMDGSDGILAWTV 180
Db 121 KKTPTVVLKATAGLRLLPEHKAALLFEVKEIFRKSFFLPVPGSVSMDGSDGILAWTV 180
Qy 181 NFLTQGLHGRQRTVGTGLDGGASTQITFLPQPEKTELEQTPRGYLTSEFNFNSTYKLYTH 240
Db 181 NFLTQGLHGRQRTVGTGLDGGASTQITFLPQPEKTELEQTPRGYLTSEFNFNSTYKLYTH 240
Qy 241 SYLGFGLKAARLATLGALETEGTDGHTFRSACLPRWLEAEWIFGGVKYQYGGNQGEVGF 300
Db 241 SYLGFGLKAARLATLGALETEGTDGHTFRSACLPRWLEAEWIFGGVKYQYGGNQGEVGF 300
Qy 301 EPCYAEVLVRVGRKHLQPEEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
Db 301 EPCYAEVLVRVGRKHLQPEEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
Qy 361 EVCDNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQ 400
Db 361 EVCDNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQ 400
Qy 421 LOSIGISH 428
Db 421 LOSIGISH 428

RESULT 3
Q8CD29 PRELIMINARY; PRT; 427 AA.
AC Q8CD29;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 5.
GN ENTPD5
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK031581; BAC27461.1; -.
DR MGD; MGI:1321385; Entpd5.
DR InterPro; IPR000407; GDAL_CD39_NTPase.
DR Pfam; PF01150; GDAL_CD39; 1.
SQ SEQUENCE 427 AA; 47101 MW; 6E3773C842B58477 CRC64;

Query Match 88.5%; Score 1990.5; DB 11; Length 427;
Best Local Similarity 88.1%; Pred. No. 9.1e-163;
Matches 376; Conservative 25; Mismatches 25; Indels 1; Gaps 1;

Qy 1 MATSWGTVFFMLVVCVCSAVSHRNQQTWPEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
Db 1 MATSWGTVFFMLVVCVCSAVSHRNQQTWPEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
Qy 61 RIHVYTFVQKMPGQPLILEGEVDSVPGLSAFVDQPKQAEIVQGLLEVAKDSIPRSHW 120
Db 61 RIHVYTFVQKMPGQPLILEGEVDSVPGLSAFVDQPKQAEIVQGLLEVAKDSIPRSHW 120
Qy 121 KKTPTVVLKATAGLRLLPEHKAALLFEVKEIFRKSFFLPVPGSVSMDGSDGILAWTV 180
Db 121 KKTPTVVLKATAGLRLLPEHKAALLFEVKEIFRKSFFLPVPGSVSMDGSDGILAWTV 180
Qy 181 NFLTQGLHGRQRTVGTGLDGGASTQITFLPQPEKTELEQTPRGYLTSEFNFNSTYKLYTH 240
Db 181 NFLTQGLHGRQRTVGTGLDGGASTQITFLPQPEKTELEQTPRGYLTSEFNFNSTYKLYTH 240
Qy 241 SYLGFGLKAARLATLGALETEGTDGHTFRSACLPRWLEAEWIFGGVKYQYGGNQGEVGF 300
Db 241 SYLGFGLKAARLATLGALETEGTDGHTFRSACLPRWLEAEWIFGGVKYQYGGNQGEVGF 300
Qy 301 EPCYAEVLVRVGRKHLQPEEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
Db 301 EPCYAEVLVRVGRKHLQPEEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
Qy 361 EVCDNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQ 400
Db 361 EVCDNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQ 400
Qy 421 LOSIGISH 427
Db 421 LOSIGISH 426
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Db 301 EPCYAEVLVRVGRKHLQPEEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
Qy 361 EVCDNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQ 400
Db 361 EVCDNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQ 400

RESULT 3
Q8CD29 PRELIMINARY; PRT; 427 AA.
AC Q8CD29;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 5.
GN ENTPD5
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK031581; BAC27461.1; -.
DR MGD; MGI:1321385; Entpd5.
DR InterPro; IPR000407; GDAL_CD39_NTPase.
DR Pfam; PF01150; GDAL_CD39; 1.
SQ SEQUENCE 427 AA; 47101 MW; 6E3773C842B58477 CRC64;

Query Match 88.5%; Score 1990.5; DB 11; Length 427;
Best Local Similarity 88.1%; Pred. No. 9.1e-163;
Matches 376; Conservative 25; Mismatches 25; Indels 1; Gaps 1;

Qy 1 MATSWGTVFFMLVVCVCSAVSHRNQQTWPEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
Db 1 MATSWGTVFFMLVVCVCSAVSHRNQQTWPEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
Qy 61 RIHVYTFVQKMPGQPLILEGEVDSVPGLSAFVDQPKQAEIVQGLLEVAKDSIPRSHW 120
Db 61 RIHVYTFVQKMPGQPLILEGEVDSVPGLSAFVDQPKQAEIVQGLLEVAKDSIPRSHW 120
Qy 121 KKTPTVVLKATAGLRLLPEHKAALLFEVKEIFRKSFFLPVPGSVSMDGSDGILAWTV 180
Db 121 KKTPTVVLKATAGLRLLPEHKAALLFEVKEIFRKSFFLPVPGSVSMDGSDGILAWTV 180
Qy 181 NFLTQGLHGRQRTVGTGLDGGASTQITFLPQPEKTELEQTPRGYLTSEFNFNSTYKLYTH 240
Db 181 NFLTQGLHGRQRTVGTGLDGGASTQITFLPQPEKTELEQTPRGYLTSEFNFNSTYKLYTH 240
Qy 241 SYLGFGLKAARLATLGALETEGTDGHTFRSACLPRWLEAEWIFGGVKYQYGGNQGEVGF 300
Db 241 SYLGFGLKAARLATLGALETEGTDGHTFRSACLPRWLEAEWIFGGVKYQYGGNQGEVGF 300
Qy 301 EPCYAEVLVRVGRKHLQPEEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
Db 301 EPCYAEVLVRVGRKHLQPEEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
Qy 361 EVCDNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQ 400
Db 361 EVCDNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQ 400
Qy 421 LOSIGISH 427
Db 421 LOSIGISH 426
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RESULT 4
Q8BR23 ID Q8BR23 PRELIMINARY; PRT; 427 AA.
AC Q8BR23;
DT 01-MAR-2003 (TEMBLrel. 23, Created)
DT 01-MAR-2003 (TEMBLrel. 23, last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 5.
GN ENTPD5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK045828; BAC32507.1; -.
DR MGD; MGI:1321385; Entpd5.
DR InterPro; IPR000407; GDA1_CD39_NTPase.
DR Pfam; PF01150; GDA1_CD39_1.
SQ SEQUENCE 427 AA; 47123 MW; 87BF2CC1CC1FCB9 CRC64;

Query Match 38.2%; Score 1984.5; DB 11; Length 427;
Best Local Similarity 87.8%; Pred. No. 3e-162;
Matches 375; Conservative 24; Mismatches 27; Indels 1; Gaps 1;

QY 1 MATSWGVFPLVVCVSAVSRNQOTWEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSWGAV-FPLIACVGSIVFREQOTWEGIFLSSMCPINVSAGTFYGIMFDAGSTGT 59
QY 61 RIHVYTFVQMPQQLPILEGEVDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSH 120
DB 60 RIHVYTFVQTAGQLPPLGEIIFDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSH 119
QY 121 KTFPVVLKATAGILPEHKAKALLPEVKEIFRKSPLVPKGSVIMDSDEGILAWTV 180
DB 120 ERTPEXLLKATAGILRLPEKAQALLPEVEEIFRNSPFLVPDGSVIMDSYEGILAWTV 179
QY 181 NPLTGQLHGRQETVGTDLGGASTQITFLPQFEKTLQTPRGYLSFEMFNSTFKLYTH 240
DB 180 NPLTGQLHGRQETVGTDLGGASTQITFLPQFEKTLQTPRGYLSFEMFNSTFKLYTH 239
QY 241 SYLGFGGLKAARLATLGALETGDTGHTFRSACLPRMLEAEWIFGGVKYQYGGNQGEGVP 300
DB 240 SYLGFGGLKAARLATLGALEAKGTGHTFRSACLPRMLEAEWIFGGVKYQYGGNQGEGVP 299
QY 301 EPCVAEVLVRVGRKLGHPPEVVGSGSFVAFSYYYDRAVDTDMDIYKGGILKVEDFERKAR 360
DB 300 EPCVAEVLVRVQGRKLGHPPEVVGSGSFVAFSYYYDRAADTHLIYKGGVILKVEDFERKAR 359
QY 361 EVCDNLNFTSGSPFLCWLDSYITALLKDGFGFADSTVLQLTKKVNNIETGVALGATFHL 420
DB 360 EVCDNLGSPSSGSPFLCWLDTYITALLKDGFGFADGTLLQLTKKVNNIETGVALGATFHL 419
QY 421 LQSLGIT 427
DB 420 LQSLGIT 426

RESULT 5
Q8TAS7 ID Q8TAS7 PRELIMINARY; PRT; 483 AA.
AC Q8TAS7;
DT 01-JUN-2002 (TEMBLrel. 21, Created)
DT 01-JUN-2002 (TEMBLrel. 21, last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 6 (Putative
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DE function).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025980; AAH25980.1; -.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR000407; GDA1_CD39_NTPase.
DR Pfam; PF01150; GDA1_CD39_1.
DR Hydrolase.
SQ SEQUENCE 483 AA; 53119 MW; A850E5035BCDCE8F CRC64;

Query Match 44.3%; Score 996; DB 4; Length 483;
Best Local Similarity 52.2%; Pred. No. 5.4e-77;
Matches 203; Conservative 57; Mismatches 123; Indels 6; Gaps 4;

QY 40 PINVSA---STLYGIMFDAGSTGTRIHYTFVQKMPGQLPILLEGVDSVKPGLSAFVDQ 96
DB 89 PLGTAADGCHVEFYGIMFDAGSTGTRHVVFQFT-RPRBTPPTLTHTFKALKPGLSAYADD 147
QY 97 PKQGAETVQGLLEVAKDSIPRSHWKTTPVLKATAGLRLPEHKAKALLFYKELFRKSP 156
DB 148 VEKSAQIGIRELLDVAKQDIPDFWKATPVLKATAGLRLPGEKAQLKQKVEFKASP 207
QY 157 FLVPKGSVIMDSDEGILAWTVNPLTQGLHGRQETVGTDLGGASTQITFLPQFEKTL 216
DB 208 FLVGDGCVSINMGTDGVSAMITINFLTCSLKTPOGSSVGMGLDGGSGTQIAFLPRVEGT 267
QY 217 LSOTPRGYLTSPEMNSTVKLYTHSYLGFGLKAARLATLGALETE-GTDTGHTFRSACLPR 275
DB 268 LQASPPGVLTALEMRNRYKLYSYLGLGLMSARLAILGGVGGPAXDKGLVSPCLSP 327
QY 276 MLEAEWIFGGVKYQYGGNQGEGVGFPCVYAEVLVRVGRKLGHPPEVVGSGSFVAFSYYYDR 335
DB 328 SFKGEWEHAEVTRYVSGOKAAASLHELCAARVSEVLQNRVHRTSEVKHVDVFAFSYYDL 387
QY 336 AVDTMDIYKGGILKVEDFERKAREVCNLENFTSGSPFLCWLDSYITALLKDGFGFAD 395
DB 388 AAGVGLIDAKGGSVLVVGDFEAAKIVCKTUSTQPSQSPSCWDLTIVSILLQE-EGFPR 446
QY 396 STVLQLTKKVNNIETGVALGATFHLIQL 424
DB 447 SKVLKLRKIDNVETSWALGAIFHVIDSL 475

RESULT 6
Q7Z5B5 ID Q7Z5B5 PRELIMINARY; PRT; 484 AA.
AC Q7Z5B5;
DT 01-OCT-2003 (TEMBLrel. 25, Created)
DT 01-OCT-2003 (TEMBLrel. 25, last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, last annotation update)
DE CD39L2 nucleotidase.
GN ENTPD6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Ivanenkov V.V., Murphy-Piedmonte D.M., Kirley T.L.;
RT "Bacterial Expression, Characterization, and Disulfide Bond
RT Determination of Soluble Human NTPDase6 (CD39L2) Nucleotidase:
RT Implications for Structure and Function."
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY327581; AAF92131.1; -.
SQ SEQUENCE 484 AA; 53274 MW; D00A5D2915DF36CE CRC64;
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Query Match 44.3%; Score 996; DB 4; Length 484;
Best Local Similarity 52.2%; Pred. No. 5.4e-77;
Matches 203; Conservative 57; Mismatches 123; Indels 6; Gaps 4;

QY 40 PINVSA---STLYGIMFDAGSTGTRHYVTVFQVQKPGQPLILEGEVDSVKGLSAFVDQ 96
DB 90 PLGTAADGHEVFYGMFDAGSTGTRVHVFOFT-RPPRETPTLTHTETFKALPKGLSAYADD 149
QY 97 PKQAGTVQGLLVAKDSIPRSHWKTTPVVKATAGLRLLFEHKAALLFEVKEIPRKPSP 156
DB 149 VKSAQGIREDLVAKQDIPDFWKATPLVKATAGLRLLPEKEAKKLQKVEKPKASP 208
QY 157 FLVPGKGSVIMDGSGLIAWTVNFLTQGLHGHROETVGTDLGASTQITFLPQPEKT 216
DB 209 FLVGGDCVSIIMGTDGVSAMITNFLTGLSKTPGGSSVGLGLGMSARLAILGGVQPAKDGKELVSPCLSP 268
QY 217 LEOTPRGYLTSPFENSTYKLYTHSYLPGKLAARLATIAGLETE-GTGHTFPRSAFLPR 275
DB 269 LQASPPGYLTALRNFRTYKLYSYLGLGMSARLAILGGVQPAKDGKELVSPCLSP 328
QY 276 WLEAEWIFGVKYQYGNQGEVGPFCYAEVLVVRGKLHQPBEVQVSGSFAPSYYYDR 335
DB 329 SFKGEWEHAEVTVRSQKAAASLHELCAARVSEVLQNRVHRTVEVKHVDYFAPSYYYDL 388
QY 336 AVDTMDIYKGGILKVEDPERKAREVCNLENFTSGSPFLCNDLSVITALLKDGFGFAD 395
DB 389 AAGVGLIDAEGKGLVGVDFEIAAKYVCRTELETQPSPPSCMDLTYVSLLLQE-FGPPR 447
QY 395 STVLQTLTKVNNIETGALGATHLLQSL 424
DB 448 SKVLKLRTRKIDNVETSWALGAIPHIDSL 476

RESULT 7
Q8N3H3 PRELIMINARY; PRT; 503 AA.
AC Q8N3H3
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein (Fragment).
GN DKF276761.915.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Amalgam.
RC SEQUENCE FROM N.A.
RA Ansong W., Winkner U., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL834158; CAD38864.1;
DR InterPro: IPR000407; GDA1_CD39_NTPase.
DR Pfam: PF01150; GDA1_CD39; 1.
KW Hypothetical protein.
FT NON TER
SQ SEQUENCE 503 AA; 54763 MW; 1639333P9139D8D9P CRC64;

Query Match 44.3%; Score 996; DB 4; Length 503;
Best Local Similarity 52.2%; Pred. No. 5.7e-77;
Matches 203; Conservative 57; Mismatches 123; Indels 6; Gaps 4;

QY 40 PINVSA---STLYGIMFDAGSTGTRHYVTVFQVQKPGQPLILEGEVDSVKGLSAFVDQ 96
DB 109 PLGTAADGHEVFYGMFDAGSTGTRVHVFOFT-RPPRETPTLTHTETFKALPKGLSAYADD 167
QY 97 PKQAGTVQGLLVAKDSIPRSHWKTTPVVKATAGLRLLFEHKAALLFEVKEIPRKPSP 156
DB 168 VKSAQGIREDLVAKQDIPDFWKATPLVKATAGLRLLPEKEAKKLQKVEKPKASP 227
QY 157 FLVPGKGSVIMDGSGLIAWTVNFLTQGLHGHROETVGTDLGASTQITFLPQPEKT 216
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DB 228 FLVGGDCVSIIMGTDGVSAMITNFLTGLSKTPGGSSVGLGLGMSARLAILGGVQPAKDGKELVSPCLSP 287
QY 217 LEOTPRGYLTSPFENSTYKLYTHSYLPGKLAARLATIAGLETE-GTGHHTFPRSAFLPR 275
DB 288 LQASPPGYLTALRNFRTYKLYSYLGLGMSARLAILGGVQPAKDGKELVSPCLSP 347
QY 276 WLEAEWIFGVKYQYGNQGEVGPFCYAEVLVVRGKLHQPBEVQVSGSFAPSYYYDR 335
DB 348 SFKGEWEHAEVTVRSQKAAASLHELCAARVSEVLQNRVHRTVEVKHVDYFAPSYYYDL 407
QY 336 AVDTMDIYKGGILKVEDPERKAREVCNLENFTSGSPFLCNDLSVITALLKDGFGFAD 395
DB 408 AAGVGLIDAEGKGLVGVDFEIAAKYVCRTELETQPSPPSCMDLTYVSLLLQE-FGPPR 466
QY 395 STVLQTLTKVNNIETGALGATHLLQSL 424
DB 467 SKVLKLRTRKIDNVETSWALGAIPHIDSL 495

RESULT 8
Q76268 PRELIMINARY; PRT; 461 AA.
AC Q76268
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NTPase protein (LD11641P).
GN NTPASE OR CG3059.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINES=20196006; PubMed=10731132;
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Efankoch C., Baldwin D.,
RA Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostler C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Nelson D.L.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kianos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zakeri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.;
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RT "The genome sequence of Drosophila melanogaster." ;
RL Science 287:2185-2195(2000).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=98341119; PubMed=9676430;
RA Chadwick B.P., Frischauf A.-M.;
RT "The CD39-like gene family: identification of three new human members
(CD39L2, CD39L3, and CD39L4), their murine homologues, and a member of
the gene family from Drosophila melanogaster." ;
RL Genomics 50:357-367(1998).
RN (3)
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayan A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuno J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celnikier S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AS003581; AAF51182.1; -
DR EMBL: AF041048; AAC39133.1; -
DR EMBL: AY061134; AAL26882.1; -
DR FlyBase; FBgn0024947; NTPase.
DR InterPro; IPR000407; GDAL_CD39_NTPase.
DR Pfam; PF01150; GDAL_CD39; 1.
SQ SEQUENCE 461 AA; 50845 MW; 27D00321F91A9DD1 CRC64;

Query Match 31.0%; Score 696.5; DB 5; Length 461;
Best Local Similarity 39.1%; Pred. No. 3.2e-51;
Matches 156; Conservative 74; Mismatches 122; Indels 47; Gaps 12;

QY 49 YGIMFDAGSTGTRIHYTVFVQKMPGQPILEGVFDVSPKGLSAFVDQPKQAGTVOGILL 108
DB 79 YAAIIDAGSTGSRVLAYKFNRSFIDNKLVLVEELPKERKFGLSFPADNPAEGAHSTKILL 138
QY 109 EVAKDSIPRSHWKTTPVVLKATAGRLLEPHKAKALLFEVKETFRKSPFLVPKGSVIMD 168
DB 139 DEARAFIPKHSWSTPLVLKATAGRLLPASKAENILNAVRLDFAKSEFSDVMDAVEIMD 198
QY 169 GSDEGILAWTVNFLTQGLHGRHQETWGTLDLGASTQTTF-----LPQEKLTLEQTP 221
DB 199 GTDEGIFSWFTVNFLLGRLSKTNQ--AAALDLGGSGTQVTFSTPDQDPQVYVVKYMHV- 255
QY 222 RGLTSEFMFNSTYKLYTHSYLGFGLKAAARLATLGALETG--TDGHTFRSACL-PRWLB 278
DB 256 ---VTSSKKIN----VFTHSYLGLGLMAARHAFV-----THGYKEDTVLESVCVNPILAN 304
QY 279 AEWIFGGVKYQYGGNQEGB-----VGPPECYAEVLVRVGRGL-----HQPEEVOGRSF 326
DB 305 RTWTYGNVQYKVGKENGKSSAEQPIVDFDAC-----LELVKSKWMLVPKPFLLKQHAV 360
QY 327 YAFSYTYDRAVDTMDIDYKGGILKVEDFERKAREVC--DNLENFTSGSPFLCMLSYIT 384
DB 361 AAFSYVFERAIBESGLVDPLAGGETTVEAVRKAQEI CAIPNDE-----QPFMCFDLTFTS 415
QY 385 ALLKDGEPADSVTLQITKKVNIETGMAWGATFHLLQS 423
DB 416 TLREGFGLDGGKKIKLYKKIDGHEISWALGCAINVLTS 454

RESULT 9
Q9VQ18 PRELIMINARY; PRT; 464 AA.
AC Q9VQ18;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, last annotation update)
DE NTPASE protein.
GN NTPASE OR CG3059.
OS Drosophila melanogaster (Fruit fly).
OC Sukarya; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Dipera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
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OX NCBI_TaxID=7227;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayan A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA Balles R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley S.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Kays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
RA Folsler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hastin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X.,
RA Svitskas R., Tector C., Turner R., Venter E., Weissenbach J.,
RA Wang Z.-Y., Wasmann D.A., Weinstock G.M., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zhao Q., Zheng L.,
RA Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhu L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster." ;
RL Science 287:2185-2195(2000).
DR EMBL: AB003581; AAF51181.1; -
DR FlyBase; FBgn0024947; NTPase.
DR InterPro; IPR000407; GDAL_CD39_NTPase.
DR Pfam; PF01150; GDAL_CD39; 1.
SQ SEQUENCE 464 AA; 51119 MW; 71D057AB85AE613D CRC64;
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Query Match 31.0%; Score 696.5; DB 5; Length 464;
Best Local Similarity 39.1%; Pred. No. 3.2e-51;
Matches 156; Conservative 74; Mismatches 122; Indels 47; Gaps 12;

QY 49 YGIMFDAGSTGTRIHYTVFVQKMPGQPILEGVFDVSPKGLSAFVDQPKQAGTVOGILL 108
DB 82 YAAIIDAGSTGSRVLAYKFNRSFIDNKLVLVEELPKERKFGLSFPADNPAEGAHSTKILL 141
QY 109 EVAKDSIPRSHWKTTPVVLKATAGRLLEPHKAKALLFEVKETFRKSPFLVPKGSVIMD 168
DB 142 DEARAFIPKHSWSTPLVLKATAGRLLPASKAENILNAVRLDFAKSEFSDVMDAVEIMD 201
QY 169 GSDEGILAWTVNFLTQGLHGRHQETWGTLDLGASTQTTF-----LPQEKLTLEQTP 221
DB 202 GTDEGIFSWFTVNFLLGRLSKTNQ--AAALDLGGSGTQVTFSTPDQDPQVYVVKYMHV- 258
QY 222 RGLTSEFMFNSTYKLYTHSYLGFGLKAAARLATLGALETG--TDGHTFRSACL-PRWLB 278
DB 259 ---VTSSKKIN----VFTHSYLGLGLMAARHAFV-----THGYKEDTVLESVCVNPILAN 307
QY 279 AEWIFGGVKYQYGGNQEGB-----VGPPECYAEVLVRVGRGL-----HQPEEVOGRSF 326
DB 308 RTWTYGNVQYKVGKENGKSSAEQPIVDFDAC-----LELVKSKWMLVPKPFLLKQHAV 363
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Qy 327 YAFSYVYDRAVDTMDIYKGGILKVEDFERKAREVC--DNLENFTSGSPFLCMLDLSYIT 384
Db 364 AAFSYFPERAIESGLVDPLAGGTTVEAYRKAQBEICAI PNDE-----QPFMCFDLTFIS 418
Qy 385 ALLKQGFADSTVLTQTKVNNIETGWCALGATFHLQOS 423
Db 419 TLLREGFLNDGKKIKYKIDGHEISWALGCAYNVLTS 457

RESULT 10
Q9XU84 PRELIMINARY; PRT; 479 AA.
ID AC Q9XU84
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE K08H10.4 protein.
GN K08H10.4
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Gardner A.E.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA none;
RX MEDLINE=99069613; PubMed=9851916;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z83113; CAB05544.1; --
DR PIR; T23508; T23508
DR WormPep; K08H10.4; C018877.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002034; AIPM/Hcit synth.
DR InterPro; IPR000407; GDAL_CD39_NTPase.
DR Pfam; PF01150; GDAL_CD39; 1.
DR PROSITE; PS00815; AIPM_HOMOCIT SYNTH 1; 1.
SQ SEQUENCE 479 AA; 53844 MW; 7EDC02A9D54A48ED CRC64;

Query Match 27.4%; Score 616.5; DB 5; Length 479;
Best Local Similarity 34.3%; Pred. No. 2.7e-44;
Matches 150; Conservative 81; Mismatches 167; Indels 39; Gaps 16;

Qy 9 FFMLVVS--CVCSAVSHRNQOTWTEGIFLSMCPINVSASTLYGIMFDAGSTGTRIHYVT 66
Db 6 FSIILLISFFSLLSVVTTKQY-WCHGDGVLN---NOHTCRFFTVIVDAGSTGTRLLHYK 60
Qy 67 FVQK-----MPQLPILEGVDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSH 119
Db 61 FIHPDPAIASHGMPEK---VEKEIFQEVKPGLSFPAKSPSSAADSLEPLQARKEVPHFM 117
Qy 120 WKTPVVLKATAGLRLLPEHKAKALLFEVK-IFRKSPFLVPKGSVIMPGSDGILAWY 178
Db 118 WEKTPITLKATAGLRLLPGMADDLISVEERIFNSGFFAAPPDAVNVMPGSDGVYSWF 177
Qy 179 TVNFLTGLH-----GHR-----QETVGTDLGGASTQITFLPQPKTELEOTPRGYLTSFE 229
Db 178 TLNLTLETLFDEFTVGHKPAHRSAVAADFLLGGSTQLTYPNNEAVPSEHV-GYERDID 236
Qy 230 MFNSTYKLYTHSYLGFLGAARLATLGALETG---TQGTFRSACLPRWLE-AEWIFGVV 286
Db 237 FFGHILRFTSFLLNGLIARLML-LQETDNEIESTHQITSCMPEGYQLTEWEY-AL 294
Qy 287 KYQYGGKQEGVGPCEVAEVLVRV-KGLHQPEEVQVGSYAFSYTYDRAVDTMDIYE 345
Db 295 KP-WNINGSSSHFSFSCVGTGKNFVSESEINHLRELKGPSYLFESYFFDRLNLSGLYKGN 353
Qy 346 KGGILKVEDFERKAREVC-----DNLENFTSGSPFLCMLDLSYITALLKQGFADSTVLQL 401
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Db 354 EGGKILKROFFKEAABIAICRREKTEIDGSHWFWOCLDTYYSLLRGYQEDNQPLVL 413
Qy 402 TKKVNNIETGWCALGATP 418
Db 414 AKKIKGMEVSWGQGLAF 430

RESULT 11
Q8CHZ3 PRELIMINARY; PRT; 278 AA.
ID AC Q8CHZ3
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DR Similar to ectonucleoside triphosphate diphosphohydrolase 6.
GN ENTPD6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Mammary gland;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC038126; AAH38126.1; --
DR MGD; MGI:1202295; Entpd6.
DR GO; GO:0015787; P:hydrolase activity; IEA.
DR InterPro; IPR000407; GDAL_CD39_NTPase.
DR Pfam; PF01150; GDAL_CD39; 1.
RX Hydrolyase.
SQ SEQUENCE 278 AA; 30130 MW; 75A92DD1AC76297F CRC64;

Query Match 26.4%; Score 593; DB 11; Length 278;
Best Local Similarity 58.0%; Pred. No. 1.2e-42;
Matches 119; Conservative 31; Mismatches 49; Indels 6; Gaps 2;

Qy 49 YGIMFDAGSTGTRIHYVTQVQKQQLPILEGVDSVKPGLSAFVDQPKQGAETVQGLL 108
Db 74 YGIMFDAGSTGTRIHYVQFA-RPPGETPTLTHTFKALPGLSAVADDVEKSAQGIQELL 132
Qy 109 EVAKOSIPRSHWKTVPVLKATAGLRLLPEHKAKALLPEVKIPFRKSPFLVPKGSVSI 168
Db 133 NVAKQHIPPYDFWRKATPLVLKATAGLRLLPEKAKQLKQKAVFKASPLVGGDCVSI 192
Qy 169 GSDEGILAVTVNFLTGLQHGHRQETVGTDLGGASTQITFLPQPKTELEOTPRGYLTSF 228
Db 193 GTDEGVSAWITVNFILGSLKTPGSSSVGMGLDGGSTQITFLPVEGTQLQASPPGHTAL 252
Qy 229 EMFNSTYKLYTHSYLGFLGAKARLA 253
Db 253 QMFNRTYKLYSYRWV-----CSRLLA 272

RESULT 12
Q9UT35 PRELIMINARY; PRT; 556 AA.
ID AC Q9UT35
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DR Putative guanosine-diphosphatase (Guanosine diphosphatase).
GN SPAC324.08 OR GDPI.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=972b-;
RC Barrell B.G., Rajandream M.A., Quail M., Seegar K., Harris D.;
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RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Sanchez R., Franco A., Notario V., Gacto M., Cansado J.;
RT "Characterization of a guanosine diphosphatase gene from
RL Schizosaccharomyces pombe.";
DR EMBL; AL121741; CAB57338.1; -
DR EMBL; AF465240; AAL69974.1; -
DR PIR; T39109; T39109.
DR GenDB SPombe; SPAC824.08; -
DR InterPro; IPR000407; GDAL_CD39_NTPase.
DR Pfam; PF01150; GDAL_CD39; 1.
DR PROSITE; PS01238; GDAL_CD39_NTPASE; 1.
SQ SEQUENCE 556 AA; 61588 MW; 1D811E3D6A6BB85 CRC64;

Query Match 23.9%; Score 538.5; DB 3; Length 556;
Best Local Similarity 34.4%; Pred. No. 1.8e-37;
Matches 144; Conservative 61; Mismatches 157; Indels 57; Gaps 13;

QY 49 YGIMFDAGSTGRIHVTYVQKMPGQLPILGEVFDVSVKPGLSAFVDPQKGAETVQGLL 108
DB 134 YVLMIDAGSTGRVHVYQNNCPNS--PKLEEFFRMIEZGLSSFAGDPEGAASLDPL 191
QY 109 EVAKOSIPRSHKKTTPVLKATAGLLELPEHKAKALLFEVKIIFRKS--PRLVPKGSVIM 167
DB 192 DYAMENVPEYRRCSEIAVKATAGLTLTGESEAKAILKSVRQHLNDYFPPIVKGVSIL 251
QY 168 DGSDEGILAWTVNFTLGOLHGH--ROETVGTLDLGASTQITFLPOFEKTLBQTPRG--- 223
DB 252 EGSMEGIYAWIINILYLTGKATHTSVAVMDLGASTQLVFPFPASDGLSDVDGKH 311
QY 224 YLTSEPMFNSTYKLYTHSYLGFLGKAARL-----ATLGALETGTGHTFRSAC 272
DB 312 YVLDYN--GEQELYQHSGLGYGLKEARKLHKFVLNNAEALKESELELG--DSTSIHPC 368
QY 273 L-----PRWLEAEWIFGVKYQYGCNCEGEVGEPCVAEVLVRV---GKLHOP 318
DB 369 LHLNASTLPDSEKSEASVFFVQPSLAHLSLQCRGIAEALYKDKNCVPCSFNGVROP 428
QY 319 ---EEVQSGSYAFSYYYDRAVDTMDIYKGGILKVEDFERKAREVC----- 363
DB 429 KFTETFTDGPILYLSFYDR-----MISLGMSTFTIEDMKVLANSVCSGPTWQDAFSL 483
QY 364 -DNLENFTSGSPFLCWDLSYITALLKDGFGFADSTVLQTKVNNIETGALGATFHL 421
DB 484 TDALKELKE-BPEWCIDLNTMISLSVGYEIPNNRQLHTAKKIDNKELGWCIGASLSML 541

RESULT 13
Q84UE0 PRELIMINARY; PRT; 455 AA.
AC Q84UE0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE Apyrase-like protein.
GN APY1.4.
OS Medicago truncatula (Barrel medic).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Eurosid I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
OX NCBI_TaxID=3880;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22531780; PubMed=12644663;
RA Navarro-Gochicoa M.T., Camut S., Niebel A., Cullimore J.V.;
RT "Expression of the Apyrase-like APY1 Genes in Roots of Medicago
RT truncatula Is Induced Rapidly and Transiently by Stress and Not by
RT Sinorhizobium meliloti or Nod Factors.";
RL Plant Physiol. 131:1124-1136(2003).
DR EMBL; AV180380; RAQ23005.1; -
DR InterPro; IPR000407; GDAL_CD39_NTPase.

DR Pfam; PF01150; GDAL_CD39; 1.
DR PROSITE; PS01238; GDAL_CD39_NTPASE; 1.
SQ SEQUENCE 455 AA; 50665 MW; 1D0A65C6A3B9B8C1 CRC64;

Query Match 23.0%; Score 518.5; DB 10; Length 455;
Best Local Similarity 32.8%; Pred. No. 6.8e-36;
Matches 151; Conservative 68; Mismatches 175; Indels 67; Gaps 17;

QY 7 TVFFMLVVSVCVSAVSHRNQCTPEGIFLSSMCPINVSASTLYGIMFDAGSTGRIHVT 66
DB 9 TTFILLMLPAITSSQYLGNLLTWKIFQKQ-----ETLTSYAVIPDAGSTGRIHVT 62
QY 67 FVQKMPGQLPIL-----EGEVFDVSVKPGLSAFVDPQKGAETVQGLLEVAKOSIPRSHWK 122
DB 63 FDQ-----NLDLHLHCNDIEFYDKIKPKGLSAYADNPQAAKSLPLLEAEADVPEDMHPK 118
QY 123 TPVVLKATAGLRLPEHKAKALLFEVKIIP--RKSPFLVPKGSVSTMDGSDGILAWTVN 181
DB 119 TPLRGATAGLRLNGDAEKILQATRMFNSRNTLVQSDAVSLIDGTQSGSYMWTVN 178
QY 182 FLTQLGHRQETVGTLDLGASTQITFLPOFEKTLBQTPR-----CYLTSFEMFNSTY 235
DB 179 YILGNLGSFTKTVGVIDLGGSVQMTYAVS--KTKAKNAPKVADGEDPYIKKLVLKGQY 237
QY 236 KLYTHSYLGFLGKAARLALTEGTDGHTFRSACLPRWLEAEWIFGVKYQYGGNQE 295
DB 238 DLYVHSYLRFGKEATRAQVLNA--TNGS-----ANPCILPGFNGFTTYSGVVEYKAFSPSS 290
QY 296 GEVGEPCVAEVLVRVGRKLPQPEVQSGSF-----YAFSYYYDRAV 337
DB 291 GS-NFNECKEIIILKVL--KNDPCYSSCTSGIWNWGGSGQKQLFVTSAPAYLVE--- 344
QY 338 DTDMDIYK--GGILKVEDFERKAREVC--NLENTS-----GSPFLCWDLSYITALL 387
DB 345 DVGAVEPNKPSILHPIDFEYAKRACALNFEDVKSTYPRLTAKRPRYVCMDDLQYHLL 404
QY 388 KDGQCFGA---DSTVLQTLTKVNN--IETGALGATFHLQSL 424
DB 405 VHGFLSPRKITVGEIGIQYQNSVVEAAWFLGTAVEAISTL 445

RESULT 14
Q8H7L6 PRELIMINARY; PRT; 489 AA.
AC Q8H7L6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Putative apyrase.
GN OSJNB0014110.10.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Saski C.,
RA Currie J., Collura K.;
RT "Rice Genomic Sequence.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AC126222; AAN65004.1; -
DR InterPro; IPR000407; GDAL_CD39_NTPase.
DR Pfam; PF01150; GDAL_CD39; 1.
DR PROSITE; PS01238; GDAL_CD39_NTPASE; 1.
SQ SEQUENCE 489 AA; 52799 MW; 0BF6BF15448BD38E CRC64;

Query Match 23.0%; Score 518.5; DB 10; Length 489;
Best Local Similarity 34.0%; Pred. No. 7.6e-36;
Matches 143; Conservative 70; Mismatches 149; Indels 59; Gaps 16;

QY 46 STLVGIMFDAGSTGRIHVTYVQKMPGQLPIL-----EGEVFDVSVKPGLSAFVDPQKGA 101
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 1, 2004, 13:41:36 ; Search time 52 Seconds
(without alignments)
2325.583 Million cell updates/sec

Title: US-10-091-085-3

Perfect score: 2250

Sequence: 1 MATSWGVPFPLVVCVCSA.....ETGWLATPHLQLSLGISH 428

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2250	100.0	428	3	AAV44849	Ray44849 Human CD3
2	2250	100.0	428	4	AAV72238	Abv72238 Human CD3
3	2250	100.0	428	4	AAV72243	Abv72243 Human CD3
4	2250	100.0	428	5	AAE19883	Aae19883 Human CD3
5	2235	99.3	428	3	AAV44850	Ray44850 Human CD3
6	2235	99.3	428	4	AAV72240	Abv72240 Human CD3
7	2104	93.5	405	3	AAV44851	Ray44851 Human CD3
8	2104	93.5	405	4	AAV72239	Abv72239 Human CD3
9	1832.5	81.4	465	5	AAE19884	Aae19884 Mouse CD3
10	1660	73.8	330	3	AAE19881	Aae19881 Human CD3
11	999	44.4	456	5	AAE19881	Aae19881 Human CD3
12	999	44.4	484	4	AAV72241	Abv72241 Human CD3
13	996	44.3	463	5	ABB06124	Abb06124 Human NS
14	996	44.3	467	5	ABJ04657	Abj04657 Protein o
15	992	44.1	456	4	AAV91929	Aam91929 Human pol
16	989	44.0	446	5	ABJ04658	Abj04658 Protein o
17	941	41.8	450	7	ADC14220	Adc14220 Human enz
18	897	39.9	462	4	AAU30882	Aau30882 Novel hum
19	819.5	36.4	471	4	AAV72242	Abv72242 Mature hu
20	696.5	31.0	461	4	ABB66213	Abb66213 Drosophil
21	696.5	31.0	464	4	ABB59611	Abb59611 Drosophil
22	590	26.2	476	3	AAV70912	Aay70912 Human CD3
23	590	26.2	476	3	RAY70889	Ray70889 Protein e
24	533	23.7	476	3	AAV70911	Aay70911 Human CD3
25	533	23.7	476	3	AAV70888	Aay70888 Protein e

26	508.5	22.6	407	7	ABW73652	Abw73652 DNA clone
27	508.5	22.6	457	7	ABW74049	Abw74049 DNA clone
28	507.5	22.6	486	2	AAW85685	Aaw85685 NBP46 roo
29	507.5	22.6	486	5	AAU78819	Aau78819 Lotus jap
30	499.5	22.2	467	2	AAW85687	Aaw85687 DBX oligo
31	498	22.1	462	2	AAW85684	Aaw85684 NBP46 roo
32	498	22.1	462	5	AAU78818	Aau78818 Dolichos
33	491.5	21.8	496	5	AAU78820	Aau78820 Medicago
34	489	21.7	455	4	AAE81952	Aae81952 Pea bligh
35	488	21.7	472	6	ABP81286	Abp81286 Arabidops
36	482.5	21.4	496	2	AAW85686	Aaw85686 NBP46 roo
37	367	16.3	495	2	AAV33296	Aay33296 Human mem
38	358.5	15.9	458	4	AAU29271	Aau29271 Human PRO
39	358.5	15.9	458	4	ABU58647	Abu58647 Human PRO
40	358.5	15.9	458	6	ABU88195	Abu88195 Novel hum
41	358.5	15.9	458	6	ABU84510	Abu84510 Human sec
42	358.5	15.9	458	6	ABR66384	AbR66384 Human sec
43	358.5	15.9	458	6	ABR65774	AbR65774 Human sec
44	358.5	15.9	458	6	ABU99714	Abu99714 Human sec
45	358.5	15.9	458	6	ABU82953	Abu82953 Human PRO

ALIGNMENTS

RESULT 1

AAV44849

ID RAY44849 standard; protein; 428 AA.

XX

AC RAY44849;

XX

DT 19-MAY-2000 (first entry)

XX

DE Human CD39-L4 protein.

XX

KW CD39-L4; human; apyrase; nucleotide diphosphatase; ND Pase;

KW ATP diphosphorylase; apyrase; adenosine diphosphate; ADP; treatment;

KW platelet aggregation; antithrombotic; thrombosis; myocardial infarction;

KW cerebral ischemia; angina; vascular graft; extracorporeal circulation;

KW molecular weight marker; nutritional supplement; tumour; prevention;

KW drug targeting; Apyrase Conserved Region; ACS.

XX Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1..22

FT Protein /label= Leader_peptide 23..428

FT /label= Mature_human_CD39-L4_protein

FT /note= Homologous to human and murine CD39"

FT Binding-site 54..58

FT Region /label= ATP_Binding_region 129..134

FT Region /label= Apyrase_Conserved_Region 169..173

FT Region /label= Apyrase_Conserved_Region 199..206

FT /note= "Conserved motif in ATPDases"

XX

XX WO200004041-A2.

XX

XX 27-JAN-2000

XX

XX 16-JUL-1999; 99WO-US016180.

XX

XX 16-JUL-1998; 98US-00118205.

XX 24-JUL-1998; 98US-00122449.

XX 04-FEB-1999; 99US-00244444.

XX 19-MAR-1999; 99US-00273447.

XX 09-JUL-1999; 99US-00350836.

XX

XX (HYSE-) HYSEQ INC.

XX

PI Ford J, Mulero JJ;
XX WPI; 2000-182397/16;
DR N-PSDB; AAZ50356, AAZ50359.
XX New nucleic acid encoding human CD39-like protein, useful for treating
PT and preventing thrombotic disease.
XX
XX
PS Claim 15; Fig 2; 125pp; English.
XX
XX The present amino acid sequence is the CD39-L4 protein, an apyrase and/or
CC nucleotide diphosphatase (NDPase). It is isolated from the human foetal
CC liver-spleen cDNA library, B2HFUS20W. It is a soluble ATP
CC diphosphohydrolases (APDase) and is involved in the hydrolysis of
CC adenosine diphosphate (ADP), the agonist that causes platelet
CC aggregation. CD39-L4 protein has 30% and 80% homology to human and murine
CC CD39. It has platelet aggregation inhibition and antithrombotic activity.
CC CD39-L4 is used to treat or prevent thrombosis, myocardial infarction,
CC cerebral ischaemia and angina. It is also used in vitro, to maintain
CC vascular grafts or during extracorporeal circulation, to hydrolyse NDP,
CC as molecular weight markers and as nutritional supplements. It is used to
CC identify therapeutic agents that bind and modulate CD39-L4. It is coupled
CC to toxins for targeting drugs to tumours or other cells that express CD39
CC -L4
XX
XX Sequence 428 AA;

Query Match 100.0%; Score 2250; DB 3; Length 428;
Best Local Similarity 100.0%; Pred. No. 3.2e-208;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATSGTGVFFMLVVCVCSAVSHRNQOTWTFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSGTGVFFMLVVCVCSAVSHRNQOTWTFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
QY 61 RIHYVTFVQKMPGQLPILEGVFDVSKPGLSAPVDQPKQGAETVQGLLEKADSI PRSHW 120
DB 61 RIHYVTFVQKMPGQLPILEGVFDVSKPGLSAPVDQPKQGAETVQGLLEKADSI PRSHW 120
QY 121 KKTVPVLKATAGLRLPEHAKALLFEVKEIFRKSPTLVKPGSVSINDGSDGELAWTV 180
DB 121 KKTVPVLKATAGLRLPEHAKALLFEVKEIFRKSPTLVKPGSVSINDGSDGELAWTV 180
QY 181 NFLAGQLGHQETVGTLDLGASTQITFLPQPEKTLQTPRGYLTSEFMFNSTYKLYTH 240
DB 181 NFLAGQLGHQETVGTLDLGASTQITFLPQPEKTLQTPRGYLTSEFMFNSTYKLYTH 240
QY 241 SYLGFGLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVYQYGGNQGEGVGF 300
DB 241 SYLGFGLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVYQYGGNQGEGVGF 300
QY 301 EPCYAEVLVRVGRKLHQPVEVQSGSFYAFSYYYDRAVDVTDMDIYKGGILKVEDFERKAR 360
DB 301 EPCYAEVLVRVGRKLHQPVEVQSGSFYAFSYYYDRAVDVTDMDIYKGGILKVEDFERKAR 360
QY 361 EVCNDLENFTSGSPFLCNDLSYITALLKXDGFGFADSTVLQLTKKNNIETGALGFHL 420
DB 361 EVCNDLENFTSGSPFLCNDLSYITALLKXDGFGFADSTVLQLTKKNNIETGALGFHL 420
QY 421 LQSLGISH 428
DB 421 LQSLGISH 428

RESULT 2
AAB72238
ID AAB72238 standard; protein; 428 AA.
XX
AC AAB72238;
XX
DT 14-MAY-2001 (first entry)
XX
DE Human CD39 like protein CD39-L4 amino acid sequence.

XX Human CD39-like protein; apyrase; NDPase; platelet function inhibitor;
KW myocardial infarction; cerebral ischaemia; angina; arterial thrombosis;
KW cerebral artery thrombosis; platelet aggregation; inflammation;
KW apoptosis; autoimmune disorder; neurological disorder;
KW Alzheimer's disease; Parkinson's disease; cancer; CD39-L4.
XX
OS Homo sapiens.
XX
XX WO200110205-A1.
XX
PD 15-FEB-2001.
XX
XX 09-AUG-2000; 2000WO-US021790.
XX
XX 09-AUG-1999; 99US-00370265.
XX 11-JAN-2000; 2000US-00481238.
XX 25-APR-2000; 2000US-00557800.
XX 26-MAY-2000; 2000US-00583231.
XX 30-JUN-2000; 2000US-00608285.
XX (HYSE-) HYSEQ INC.
XX
XX Ford J, Mulero JJ, Yeung G;
XX
XX WPI; 2001-147489/15.
XX N-PSDB; AAF63383.
XX
XX Polynucleotides encoding human CD39-like polypeptides, with apyrase
PT and/or NDPase activity, which are useful in the treatment of pathological
PT conditions caused by thrombosis (e.g. myocardial infarction) and
PT inflammatory disorders.
XX
XX Claim 15; Fig 2; 203pp; English.
XX
XX This invention relates to polynucleotides encoding human CD39-like
CC polypeptides with apyrase and/or NDPase activity. The polypeptides having
CC APDase, including NDPase, activity are useful for inhibiting platelet
CC function and can therefore be used in the prophylaxis or treatment of
CC pathological conditions caused by or involving thrombosis or excessive
CC coagulation or excessive platelet aggregation, such as myocardial
CC infarction, cerebral ischaemia, angina, arterial thrombosis, cerebral
CC artery thrombosis or intracardiac thrombosis, and conditions associated
CC with venous thrombosis. CD39-L4 and CD39-L2 polypeptides are useful in
CC modulating disease states (including platelet aggregation, inflammation
CC and apoptosis) associated with ADP or other purinergic signalling by
CC reducing the levels of NDPs. The polypeptides are also useful for
CC prophylaxis or treatment of inflammatory related disorders, such as
CC disorders involving sepsis or systemic inflammatory response syndrome or
CC SIRS (and associated conditions such as fever, tachycardia, tachypnea,
CC cytokine overstimulation); autoimmune disorders such as thrombosis,
CC atherosclerosis, acute pancreatitis, dermatitis, including psoriasis,
CC cirrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis;
CC neurological disorders including neurodegenerative diseases, epilepsy,
CC depression, Alzheimer's disease, Parkinson's disease, Huntington's
CC disease, and amyotrophic lateral sclerosis; and cancer. The present
CC sequence represents human CD39 like protein CD39-L4
XX
XX Sequence 428 AA;

Query Match 100.0%; Score 2250; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 3.2e-208;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATSGTGVFFMLVVCVCSAVSHRNQOTWTFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSGTGVFFMLVVCVCSAVSHRNQOTWTFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
QY 61 RIHYVTFVQKMPGQLPILEGVFDVSKPGLSAPVDQPKQGAETVQGLLEKADSI PRSHW 120
DB 61 RIHYVTFVQKMPGQLPILEGVFDVSKPGLSAPVDQPKQGAETVQGLLEKADSI PRSHW 120
QY 121 KKTVPVLKATAGLRLPEHAKALLFEVKEIFRKSPTLVKPGSVSINDGSDGELAWTV 180

DB 121 KKTVPVVKATAGLRLPEHAKALLFEVKEIFRKSPLVPKGSVIMDSDEGILAWTV 180
 QY 181 NLTGQLHGHROBTGTDLGGASTQITLPOPEKTEQTPRGYLTSPFEMNSTYKLYTH 240
 DB 181 NLTGQLHGHROBTGTDLGGASTQITLPOPEKTEQTPRGYLTSPFEMNSTYKLYTH 240
 QY 241 SYLGFLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGYKYQYGNQGEVGF 300
 DB 241 SYLGFLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGYKYQYGNQGEVGF 300
 QY 301 EPCYAEVLVRVGRKLHQPVEVQSGFYAFSYYYDRAVDMDIDYKGGILKVEDPERKAR 360
 DB 301 EPCYAEVLVRVGRKLHQPVEVQSGFYAFSYYYDRAVDMDIDYKGGILKVEDPERKAR 360
 QY 361 EVCNLENFTSGSPFLCMLDLSYITALLKDGFGFADSTVLQTKKVNNIETGALGATPHL 420
 DB 361 EVCNLENFTSGSPFLCMLDLSYITALLKDGFGFADSTVLQTKKVNNIETGALGATPHL 420
 QY 421 LQSLGISH 428
 DB 421 LQSLGISH 428

RESULT 3
 AAB72243
 ID AAB72243 standard; protein; 428 AA.
 AC AAB72243;
 XX
 XX
 DT 14-MAY-2001 (first entry)
 DE Human CD39 like protein CD39-L4 amino acid sequence.

XX Human CD39-like protein; apyrase; NDPase; platelet function inhibitor;
 XX myocardial infarction; cerebral ischaemia; angina; arterial thrombosis;
 KW cerebral artery thrombosis; platelet aggregation; inflammation;
 KW apoptosis; autoimmune disorder; neurological disorder;
 KW Alzheimer's disease; Parkinson's disease; cancer; CD39-L4.
 XX Homo sapiens.
 XX WO200110205-A1.
 XX
 XX 15-FEB-2001.
 XX 09-AUG-2000; 2000WO-US021790.
 XX
 XX 09-AUG-1999; 99US-00370265.
 PR 11-JAN-2000; 2000US-00481238.
 PR 25-APR-2000; 2000US-00557800.
 PR 26-MAY-2000; 2000US-00583231.
 PR 30-JUN-2000; 2000US-00608285.
 XX (HYSB-) HYSEQ INC.
 XX
 XX Ford J, Mulero JJ, Yeung G;
 XX WPI; 2001-147489/15.
 XX N-PSDB; AAF63402.
 XX
 XX Polynucleotides encoding human CD39-like polypeptides, with apyrase
 PT and/or NDPase activity, which are useful in the treatment of pathological
 PT conditions caused by thrombosis (e.g. myocardial infarction) and
 PT inflammatory disorders.
 XX
 XX Example 9; Page 142-144; 203pp; English.
 PS
 XX This invention relates to polynucleotides encoding human CD39-like
 CC polypeptides with apyrase and/or NDPase activity. The polypeptides having
 CC ATPase, including NDPase, activity are useful for inhibiting platelet
 CC function and can therefore be used in the prophylaxis or treatment of
 CC pathological conditions caused by or involving thrombosis or excessive

CC coagulation or excessive platelet aggregation, such as myocardial
 CC infarction, cerebral ischaemia, angina, arterial thrombosis, cerebral
 CC artery thrombosis or intracardiac thrombosis, and conditions associated
 CC with venous thrombosis. CD39-L4 and CD39-L2 polypeptides are useful in
 CC modulating disease states (including platelet aggregation, inflammation
 CC and apoptosis) associated with ADP or other purinergic signalling by
 CC reducing the levels of NDPs. The polypeptides are also useful for
 CC prophylaxis or treatment of inflammation related disorders, such as
 CC disorders involving sepsis or systemic inflammatory response syndrome or
 CC SIRS (and associated conditions such as fever, tachycardia, tachypnea,
 CC cytokine overstimulation); autoimmune disorders such as thrombosis,
 CC atherosclerosis, acute pancreatitis, dermatitis, including psoriasis,
 CC cirrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis;
 CC neurological disorders including neurodegenerative diseases, epilepsy,
 CC depression, Alzheimer's disease, Parkinson's disease, Huntington's
 CC disease, and amyotrophic lateral sclerosis; and cancer. The present
 CC sequence represents the CD39 like protein CD39-L4 amino acid sequence
 XX
 SQ Sequence 428 AA;

Query Match 100.0%; Score 2250; DB 4; Length 428;
 Best Local Similarity 100.0%; Pred. No. 3.2e+208;
 Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATSWGTVFFMLVWVCVCSAVSHRNQQTWFGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
 DB 1 MATSWGTVFFMLVWVCVCSAVSHRNQQTWFGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
 QY 61 RIHVYTFVQKMPGQLPILLEGVDSVKPGLSAFVDOPKQAGTVOGLEVAKDSIPRSHW 120
 DB 61 RIHVYTFVQKMPGQLPILLEGVDSVKPGLSAFVDOPKQAGTVOGLEVAKDSIPRSHW 120
 QY 121 KKTVPVVKATAGLRLPEHAKALLFEVKEIFRKSPLVPKGSVIMDSDEGILAWTV 180
 DB 121 KKTVPVVKATAGLRLPEHAKALLFEVKEIFRKSPLVPKGSVIMDSDEGILAWTV 180
 QY 181 NLTGQLHGHROBTGTDLGGASTQITLPOPEKTEQTPRGYLTSPFEMNSTYKLYTH 240
 DB 181 NLTGQLHGHROBTGTDLGGASTQITLPOPEKTEQTPRGYLTSPFEMNSTYKLYTH 240
 QY 241 SYLGFLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGYKYQYGNQGEVGF 300
 DB 241 SYLGFLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGYKYQYGNQGEVGF 300
 QY 301 EPCYAEVLVRVGRKLHQPVEVQSGFYAFSYYYDRAVDMDIDYKGGILKVEDPERKAR 360
 DB 301 EPCYAEVLVRVGRKLHQPVEVQSGFYAFSYYYDRAVDMDIDYKGGILKVEDPERKAR 360
 QY 361 EVCNLENFTSGSPFLCMLDLSYITALLKDGFGFADSTVLQTKKVNNIETGALGATPHL 420
 DB 361 EVCNLENFTSGSPFLCMLDLSYITALLKDGFGFADSTVLQTKKVNNIETGALGATPHL 420
 QY 421 LQSLGISH 428
 DB 421 LQSLGISH 428

RESULT 4
 AAE19883
 ID AAE19883 standard; protein; 428 AA.
 XX
 AC AAE19883;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Human CD39L4 protein.
 XX Human; CD39L4 protein; therapy; immune deficiency;
 KW autoimmune disorder; multiple sclerosis; systemic lupus erythematosus;
 KW rheumatoid arthritis; autoimmune thyroiditis; allergic reaction; asthma;
 KW insulin dependent diabetes mellitus; periodontal disease; osteoporosis;
 KW osteoarthritis; wound healing; tissue repair; Alzheimer's disease; ulcer;
 KW Parkinson's disease; amyotrophic lateral sclerosis; Huntington's disease;

nervous system disease; nerve injury; ischaemia-reperfusion injury; endotoxin lethality; arthritis; nephritis; inflammatory bowel disease; Crohn's disease; virucide; antibacterial; antifungal; neuroprotective; dermatological; immunosuppressive; vulnery; nootropic; anticonvulsant; antiinflammatory; nephrotropic; gastrointestinal; vasotropic.

OS Homo sapiens.
XX USG350447-B1.
XX 26-FEB-2002.
XX 29-JAN-1999; 99US-00240639.
XX 29-JAN-1999; 99US-00240639.
XX (HYSE-) HYSEQ INC.
XX Chadwick BP, Frischauf A;
XX MPI, 2002-215262/27.
XX N-PSDB; AAD31695.

An isolated polypeptide with phosphohydrolase activity, designated CD39L2, useful to identify other proteins with which binding occurs or identify inhibitors and for treatment of, e.g., Alzheimer's, multiple sclerosis and osteoporosis.

XX Example; Fig 7; 10pp; English.

The present invention relates to novel proteins with phosphohydrolase activity, designated CD-39-like (CD39L) proteins and polynucleotides encoding such proteins. CD39L proteins are useful to treat infectious diseases caused by viral, bacterial, fungal or other infection that may be treatable with CD39L. They are useful in the treatment of various immune deficiencies and disorders, autoimmune disorders such as multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune thyroiditis and insulin dependent diabetes mellitus, allergic reactions and conditions such as asthma and other respiratory problems, periodontal disease, osteoporosis, osteoarthritis and other tooth repair processes. They may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration as well as for wound healing and tissue repair and replacement and in the treatment of burns, incisions and ulcers. CD39L proteins may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central nervous system diseases such as Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, Huntington's disease, peripheral nervous system diseases peripheral nerve injuries, peripheral neuropathy and localised neuropathies. They are also used to treat mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. CD39L proteins of the invention are also useful to promote better or faster closure of non-healing wounds, including pressure ulcers, ulcers associated with vascular insufficiency and surgical and traumatic wounds. They also exhibit anti-inflammatory activity and may be used to treat inflammatory conditions including chronic or acute conditions, including ischaemia-reperfusion injury, endotoxin lethality, arthritis, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease or Crohn's disease. The present sequence is human CD39L4 protein

Sequence 428 AA;
Query Match 100.0%; Score 2250; DB 5; Length 428;
Best Local Similarity 100.0%; Pred. No. 3.2e-208; Gaps 0;
Matches 428; Conservative 0; Mismatches 0; Indels 0;

QY 1 MATSGTGVFFMLVWSCVCSAVSHRNQQTWTFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
Db 1 MATSGTGVFFMLVWSCVCSAVSHRNQQTWTFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
QY 61 RIHYTVFVQKMPQQLPILEGVDFSVKGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
Db 61 RIHYTVFVQKMPQQLPILEGVDFSVKGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120

QY 121 KKTTPVVLKATAGRLLEPEKAKALLPEVKEIFRKSPLVPKGSVIMDSGDEGILAWTV 180
Db 121 KKTTPVVLKATAGRLLEPEKAKALLPEVKEIFRKSPLVPKGSVIMDSGDEGILAWTV 180
QY 181 NLTGQQLHGRQETVGTDLGGASTQITLPOPEKTLBOTPRGYLTSFEMENSTYKLYTH 240
Db 181 NLTGQQLHGRQETVGTDLGGASTQITLPOPEKTLBOTPRGYLTSFEMENSTYKLYTH 240
QY 241 SYLGFGKKAARLATLGALETEGTDGHTFRSACLPRWLEAEWIFGGVYKYQYGGNOGEVGF 300
Db 241 SYLGFGKKAARLATLGALETEGTDGHTFRSACLPRWLEAEWIFGGVYKYQYGGNOGEVGF 300
QY 301 EPCYAEVLVVRGKLHQPBEVQVGSYAFSYVDRAVDMDIDYKGGILKVEDDFPKAR 360
Db 301 EPCYAEVLVVRGKLHQPBEVQVGSYAFSYVDRAVDMDIDYKGGILKVEDDFPKAR 360
QY 361 EVCDNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQLTKKVNNIETGMALGATFHL 420
Db 361 EVCDNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQLTKKVNNIETGMALGATFHL 420
QY 421 LQSLGISH 428
Db 421 LQSLGISH 428

RESULT 5
AAY44850
ID AAY44850 standard; protein; 428 AA.
XX AC AAY44850;
XX 18-MAY-2000 (first entry)
XX Human CD39-L4 variant-ACR III mutant protein.
XX CD39-L4; human; apyrase; nucleotide diphosphatase; NDPase; variant;
XX ATP diphosphohydrolase; APBbase; adenosine diphosphate; ADP; treatment;
XX platelet aggregation; antithrombotic; thrombosis; myocardial infarction;
XX cerebral ischaemia; angina; vascular graft; extracorporeal circulation;
XX molecular weight marker; nutritional supplement; tumour; prevention;
XX drug targeting; substitution mutation.
XX Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
XX Misc-difference 168 /note= "Wild type Asp substituted with Thr"
XX Misc-difference 170 /note= "Wild type Ser substituted with Gln"
XX Misc-difference 175 /note= "Wild type Leu substituted with Phe"
XX WO200004041-A2.
XX 27-JAN-2000.
XX 16-JUL-1999; 99WO-US016180.
XX 16-JUL-1998; 98US-00118205.
XX 24-JUL-1998; 98US-00122449.
XX 04-FEB-1999; 99US-00244444.
XX 19-MAR-1999; 99US-00273447.
XX 09-JUL-1999; 99US-00350836.
XX (HYSE-) HYSEQ INC.
XX Ford J, Mulero J;
XX WPI; 2000-182397/16.
XX N-PSDB; AAZ50357.

PT New nucleic acid encoding human CD39-like protein, useful for treating
 PT and preventing thrombotic disease.
 PS Claim 17; Fig 6; 125pp; English.
 XX
 XX The present amino acid sequence is the CD39-L4 variant, designated as ACR
 CC III mutant protein, an apyrase and/or nucleotide diphosphatase (NDPase).
 CC It is isolated from the human foetal liver-spleen cDNA library,
 CC b2HFTS20W. It is a soluble ATP diphosphohydrolase (ATPase) and is
 CC involved in the hydrolysis of adenosine diphosphate (ADP), the agonist
 CC that causes platelet aggregation. CD39-L4 protein has 30% and 80%
 CC homology to human and murine CD39. It has platelet aggregation inhibition
 CC and antithrombotic activity. CD39-L4 is used to treat or prevent
 CC thrombosis, myocardial infarction, cerebral ischaemia and angina. It is
 CC also used in vitro, to maintain vascular grafts or during extracorporeal
 CC circulation, to hydrolyse NDP, as molecular weight markers and as
 CC nutritional supplements. It is used to identify therapeutic agents that
 CC bind and modulate CD39-L4. It is coupled to toxins for targeting drugs to
 CC tumours or other cells that express CD39-L4
 XX
 XX Sequence 428 AA;
 SQ
 Query Match 99.3%; Score 2235; DB 3; Length 428;
 Best Local Similarity 99.3%; Pred. No. 9e-207;
 Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MATSWGTVFVPMVSVCSAVSHRNQQTWFEGLFLSSMCPINVSASTLYGIMFDAGSTGT 60
 DB 1 MATSWGTVFVPMVSVCSAVSHRNQQTWFEGLFLSSMCPINVSASTLYGIMFDAGSTGT 60
 QY 61 RIHVYTFVQMPGQLPILEGVFDVSKPGLSAFVDPKQGAETVQGLLEVAKDSIPRSHW 120
 DB 61 RIHVYTFVQMPGQLPILEGVFDVSKPGLSAFVDPKQGAETVQGLLEVAKDSIPRSHW 120
 QY 121 KTFPVVLKATAGRLRLPEHKAKALLFEVKIIFRKSPLVPGKSVSMDGSDGILAWTV 180
 DB 121 KTFPVVLKATAGRLRLPEHKAKALLFEVKIIFRKSPLVPGKSVSMDGSDGILAWTV 180
 QY 121 KTFPVVLKATAGRLRLPEHKAKALLFEVKIIFRKSPLVPGKSVSMDGSDGILAWTV 180
 DB 121 KTFPVVLKATAGRLRLPEHKAKALLFEVKIIFRKSPLVPGKSVSMDGSDGILAWTV 180
 QY 181 NFLTQGLHGRQETVGTGLDGGASTQITFLPQEKLEQTPRGYLFSPFMFNSTYKLYTH 240
 DB 181 NFLTQGLHGRQETVGTGLDGGASTQITFLPQEKLEQTPRGYLFSPFMFNSTYKLYTH 240
 QY 241 SYLGFGKLAARLATLGALETGDTGHTFRSACLPRMLEAWIFGGVVKYQVGGNQEVEGF 300
 DB 241 SYLGFGKLAARLATLGALETGDTGHTFRSACLPRMLEAWIFGGVVKYQVGGNQEVEGF 300
 QY 301 EPCYAEVLVRVKGILHOPERVQGSFVAFSYVDRAVDTDMIDYKGGILKVEDFERKAR 360
 DB 301 EPCYAEVLVRVKGILHOPERVQGSFVAFSYVDRAVDTDMIDYKGGILKVEDFERKAR 360
 QY 361 EVCNDLENFTSGSPFLCWDLSYITALLKDGFGFADSTVLQITKKVNNIETGMALGATFHL 420
 DB 361 EVCNDLENFTSGSPFLCWDLSYITALLKDGFGFADSTVLQITKKVNNIETGMALGATFHL 420
 QY 421 LQSLGISH 428
 DB 421 LQSLGISH 428
 RESULT 6
 AAB72240
 ID AAB72240 standard; protein; 428 AA.
 XX
 AC AAB72240;
 XX
 DT 14-MAY-2001 (first entry)
 XX
 DE Human CD39 like protein CD39-L4 variant ACRIII amino acid sequence.
 XX
 KW Human CD39-like protein; apyrase; NDPase; platelet function inhibitor;
 KW myocardial infarction; cerebral ischaemia; angina; arterial thrombosis;
 KW cerebral artery thrombosis; platelet aggregation; inflammation;
 KW apoptosis; autoimmune disorder; neurological disorder; mutant; mutein;

KW Alzheimer's disease; Parkinson's disease; cancer; CD39-L4.
 XX Homo sapiens.
 XX WO200110205-A1.
 XX 15-FEB-2001.
 XX 09-AUG-2000; 2000WO-US021790.
 XX 09-AUG-1999; 99US-00370265.
 XX 11-JAN-2000; 2000US-00481238.
 XX 25-APR-2000; 2000US-00557800.
 XX 28-MAY-2000; 2000US-00583231.
 XX 30-JUN-2000; 2000US-00608285.
 XX (HYSE-) HYSEQ INC.
 XX Ford J, Mulero JJ, Yeung G;
 XX WPI; 2001-147489/15.
 XX N-PSDB; AAF63385.
 XX Polynucleotides encoding human CD39-like polypeptides, with apyrase
 PT and/or NDPase activity, which are useful in the treatment of pathological
 PT conditions caused by thrombosis (e.g. myocardial infarction) and
 PT inflammatory disorders.
 XX Claim 19; Fig 6; 203pp; English.
 XX This invention relates to polynucleotides encoding human CD39-like
 CC polypeptides with apyrase and/or NDPase activity. The polypeptides having
 CC ATPase, including NDPase, activity are useful for inhibiting platelet
 CC function and can therefore be used in the prophylaxis or treatment of
 CC pathological conditions caused by or involving thrombosis or excessive
 CC coagulation or excessive platelet aggregation, such as myocardial
 CC infarction, cerebral ischaemia, angina, arterial thrombosis, cerebral
 CC artery thrombosis or intracardiac thrombosis, and conditions associated
 CC with venous thrombosis. CD39-L4 and CD39-L2 polypeptides are useful in
 CC modulating disease states (including platelet aggregation, inflammation
 CC and apoptosis) associated with ADP or other purineergic signalling by
 CC reducing the levels of NDPs. The polypeptides are also useful for
 CC prophylaxis or treatment of inflammation related disorders, such as
 CC disorders involving sepsis or systemic inflammatory response syndrome or
 CC SIRS (and associated conditions such as fever, tachycardia, tachypnea,
 CC cytokine overstimulation); autoimmune disorders such as thrombosis,
 CC atherosclerosis, acute pancreatitis, dermatitis, including psoriasis,
 CC cirrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis;
 CC neurological disorders including neurodegenerative diseases, epilepsy,
 CC depression, Alzheimer's disease, Parkinson's disease, Huntington's
 CC disease, and amyotrophic lateral sclerosis; and cancer. The present
 CC sequence represents human CD39 like protein CD39-L4 variant ACRIII
 XX Sequence 428 AA;
 SQ
 Query Match 99.3%; Score 2235; DB 4; Length 428;
 Best Local Similarity 99.3%; Pred. No. 9e-207;
 Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MATSWGTVFVPMVSVCSAVSHRNQQTWFEGLFLSSMCPINVSASTLYGIMFDAGSTGT 60
 DB 1 MATSWGTVFVPMVSVCSAVSHRNQQTWFEGLFLSSMCPINVSASTLYGIMFDAGSTGT 60
 QY 61 RIHVYTFVQMPGQLPILEGVFDVSKPGLSAFVDPKQGAETVQGLLEVAKDSIPRSHW 120
 DB 61 RIHVYTFVQMPGQLPILEGVFDVSKPGLSAFVDPKQGAETVQGLLEVAKDSIPRSHW 120
 QY 121 KTFPVVLKATAGRLRLPEHKAKALLFEVKIIFRKSPLVPGKSVSMDGSDGILAWTV 180
 DB 121 KTFPVVLKATAGRLRLPEHKAKALLFEVKIIFRKSPLVPGKSVSMDGSDGILAWTV 180
 QY 181 NFLTQGLHGRQETVGTGLDGGASTQITFLPQEKLEQTPRGYLFSPFMFNSTYKLYTH 240
 DB 181 NFLTQGLHGRQETVGTGLDGGASTQITFLPQEKLEQTPRGYLFSPFMFNSTYKLYTH 240

Db 181 NLTGQLHGRQETVGLDGGASTQITLPPQFEKTLQTPRGYLTSFEMFNSTYKLYTH 240
Qy 241 SYLGFGLKAARLATLGALETGTGHTFRSACLPRWLEAEKIFGGVKYQYGGNQGEVGF 300
Db 241 SYLGFGLKAARLATLGALETGTGHTFRSACLPRWLEAEKIFGGVKYQYGGNQGEVGF 300
Qy 301 EPCYAEVLVRVGRKQHPEEVQVGSFVAFSYYYDRAVDVTMDIYKGGILKVEDFERKAR 360
Db 301 EPCYAEVLVRVGRKQHPEEVQVGSFVAFSYYYDRAVDVTMDIYKGGILKVEDFERKAR 360
Qy 361 EVCNDLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQLTKKVNNIETGWLGAFTHL 420
Db 361 EVCNDLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQLTKKVNNIETGWLGAFTHL 420
Qy 421 LOSLGISH 428
Db 421 LOSLGISH 428

RESULT 7

AAV44851
ID AAV44851 standard; protein; 405 AA.
AC AAV44851;
XX
DT 18-MAY-2000 (first entry)
XX
DE Human CD39-L66 protein.
XX
KW CD39-L6; human; CD39-L66; apyrase; nucleotide diphosphatase; NDPase;
KW ATP diphosphohydrolase; ATPase; adenosine diphosphate; ADP; treatment;
KW platelet aggregation; antithrombotic; thrombosis; myocardial infarction;
KW cerebral ischaemia; angina; vascular graft; extracorporeal circulation;
KW molecular weight marker; nutritional supplement; tumour; prevention;
KW drug targeting; splice variant.
XX
OS Homo sapiens.
XX
PN WO200004041-A2.
XX
PD 27-JAN-2000.
XX
PF 16-JUL-1999; 99WO-US016180.
XX
PR 16-JUL-1999; 98US-00118205.
PR 24-JUL-1998; 98US-00112249.
PR 04-FEB-1999; 99US-0024444.
PR 19-MAR-1999; 99US-00273447.
PR 09-JUL-1999; 99US-00350836.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Ford J, Mulero JJ;
XX
XX WPI; 2000-182397/16.
XX N-PSDB; AAZ50358.
XX
PT New nucleic acid encoding human CD39-like protein, useful for treating
PT and preventing thrombotic disease.
XX
XX Claim 15; Page 124-125; 125pp; English.

XX The present amino acid sequence is the CD39-L66 protein, a splice variant
XX of the CD39-L4 protein. It is an apyrase and/or nucleotide diphosphatase
XX (NDPase), isolated from the human foetal liver-spleen cDNA library,
XX b2HLIS20W. It is a soluble ATP diphosphohydrolase (ATPDase) and is
XX involved in the hydrolysis of adenosine diphosphate (ADP), the agonist
XX that causes platelet aggregation. CD39-L4 protein has 30% and 80%
XX homology to human and murine CD39. It has platelet aggregation inhibition
XX and antithrombotic activity. CD39-L4 is used to treat or prevent
XX thrombosis, myocardial infarction, cerebral ischaemia and angina. It is
XX also used in vitro, to maintain vascular grafts or during extracorporeal
XX circulation, to hydrolyse NDP, as molecular weight markers and as

CC nutritional supplements. It is used to identify therapeutic agents that
CC bind and modulate CD39-L4. It is coupled to toxins for targeting drugs to
CC tumours or other cells that express CD39-L4
XX
SQ Sequence 405 AA;
Query Match 93.5%; Score 2104; DB 3; Length 405;
Best Local Similarity 100.0%; Pred. No. 3.7e-194;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MATSWGTVFVFLVWVSCSAVSHRNQQTWPEGIFLSSMCPINVSASTLYGIMPDAGSTGT 60
Db 1 MATSWGTVFVFLVWVSCSAVSHRNQQTWPEGIFLSSMCPINVSASTLYGIMPDAGSTGT 60
Qy 61 RIHYTTFVQKMPQQLPILEGSEVFDVSKPGLSAFVDPQKQGAETVQGLLEVAKDSIPRSHW 120
Db 61 RIHYTTFVQKMPQQLPILEGSEVFDVSKPGLSAFVDPQKQGAETVQGLLEVAKDSIPRSHW 120
Qy 121 KKTSPVVLKATAGLRLLPEHAKALLFEVKEIIFKSPFLVPGKGSVSIKDSDEGILAWTV 180
Db 121 KKTSPVVLKATAGLRLLPEHAKALLFEVKEIIFKSPFLVPGKGSVSIKDSDEGILAWTV 180
Qy 181 NFLTQGLHGRQETVGLDGGASTQITLPPQFEKTLQTPRGYLTSFEMFNSTYKLYTH 240
Db 181 NFLTQGLHGRQETVGLDGGASTQITLPPQFEKTLQTPRGYLTSFEMFNSTYKLYTH 240
Qy 241 SYLGFGLKAARLATLGALETGTGHTFRSACLPRWLEAEKIFGGVKYQYGGNQGEVGF 300
Db 241 SYLGFGLKAARLATLGALETGTGHTFRSACLPRWLEAEKIFGGVKYQYGGNQGEVGF 300
Qy 301 EPCYAEVLVRVGRKQHPEEVQVGSFVAFSYYYDRAVDVTMDIYKGGILKVEDFERKAR 360
Db 301 EPCYAEVLVRVGRKQHPEEVQVGSFVAFSYYYDRAVDVTMDIYKGGILKVEDFERKAR 360
Qy 361 EVCNDLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQ 400
Db 361 EVCNDLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQ 400

RESULT 8

AAV72239
ID AAV72239 standard; protein; 405 AA.
XX
AC AAV72239;
XX
DT 14-MAY-2001 (first entry)
XX
DE Human CD39 like protein CD39-L4 amino acid sequence.
XX
KW Human CD39-like protein; apyrase; NDPase; platelet function inhibitor;
KW myocardial infarction; cerebral ischaemia; angina; arterial thrombosis;
KW cerebral artery thrombosis; platelet aggregation; inflammation;
KW apoptosis; autoimmune disorder; neurological disorder;
KW Alzheimer's disease; Parkinson's disease; cancer; CD39-L4.
XX
OS Homo sapiens.
XX
XX WO200110205-A1.
XX
XX 15-FEB-2001.
XX
XX 09-AUG-2000; 2000WO-US021790.
XX
XX 09-AUG-1999; 99US-00370265.
XX 11-JAN-2000; 2000US-00481238.
XX 25-APR-2000; 2000US-00557800.
XX 26-MAY-2000; 2000US-00583231.
XX 30-JUN-2000; 2000US-00608285.
XX (HYSE-) HYSEQ INC.
XX Ford J, Mulero JJ, Yeung G;
XX

DR WPI: 2001-147489/15.
DR N-PSDB; AAF63384.
XX
PT Polynucleotides encoding human CD39-like polypeptides, with apyrase
PT and/or NTPase activity, which are useful in the treatment of pathological
PT conditions caused by thrombosis (e.g. myocardial infarction) and
PT inflammatory disorders.
XX
PS
PS Claim 17: Page 157-158; 203pp; English.
XX
CC This invention relates to polynucleotides encoding human CD39-like
CC polypeptides with apyrase and/or NTPase activity. The polypeptides having
CC Apyrase, including NTPase, activity are useful for inhibiting platelet
CC function and can therefore be used in the prophylaxis or treatment of
CC pathological conditions caused by or involving thrombosis or excessive
CC coagulation or excessive platelet aggregation, such as myocardial
CC infarction, cerebral ischemia, angina, arterial thrombosis, cerebral
CC artery thrombosis or intracardiac thrombosis and conditions associated
CC with venous thrombosis. CD39-L4 and CD39-L2 polypeptides are useful in
CC modulating disease states (including platelet aggregation, inflammation
CC and apoptosis) associated with ADP or other purinergic signalling by
CC reducing the levels of NTPs. The polypeptides are also useful for
CC prophylaxis or treatment of inflammation related disorders, such as
CC disorders involving sepsis or systemic inflammatory response syndrome or
CC SIRS (and associated conditions such as fever, tachycardia, tachypnea,
CC cytokine overstimulation); autoimmune disorders such as thrombosis,
CC atherosclerosis, acute pancreatitis, dermatitis, including psoriasis,
CC cirrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis,
CC neurological disorders including neurodegenerative diseases, epilepsy,
CC depression, Alzheimer's disease, Parkinson's disease, Huntington's
CC disease, and amyotrophic lateral sclerosis; and cancer. The present
CC sequence represents human CD39 like protein CD39-L4
XX
SQ Sequence 405 AA;

Query Match 93.5%; Score 2104; DB 4; Length 405;
Best Local Similarity 100.0%; Pred. No. 3.7e-194;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MATSWGTVPMLVVCVCSAVSHRNQOTWPEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSWGTVPMLVVCVCSAVSHRNQOTWPEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
QY 61 RIHYVTFVQKMPQLPLEGEVDSVKPGLSAFVDPKQGAETVQGLLEVAKDSIPRSHW 120
DB 61 RIHYVTFVQKMPQLPLEGEVDSVKPGLSAFVDPKQGAETVQGLLEVAKDSIPRSHW 120
QY 121 KKTPTVVLKATAGLRLPEHKAKALLFEVKIIFPKSPFLPKGSVIMDSDEGILAWTV 180
DB 121 KKTPTVVLKATAGLRLPEHKAKALLFEVKIIFPKSPFLPKGSVIMDSDEGILAWTV 180
QY 181 NPLTGQLHGRQETVGTLDLGGASTQITFLPQEKLETPPGYLTSPFENSTYKLYTH 240
DB 181 NPLTGQLHGRQETVGTLDLGGASTQITFLPQEKLETPPGYLTSPFENSTYKLYTH 240
QY 241 SYLFGGLKAARLATGALETGTGHTFRSACLPRWLEAWIPFGVKYQYGGNQEVEGF 300
DB 241 SYLFGGLKAARLATGALETGTGHTFRSACLPRWLEAWIPFGVKYQYGGNQEVEGF 300
QY 301 EPCYAEVLVRGKLHPREVORGSFYASYYYDRAVDMDIDYKGGILKVEDFERKAR 360
DB 301 EPCYAEVLVRGKLHPREVORGSFYASYYYDRAVDMDIDYKGGILKVEDFERKAR 360
QY 361 EVCNDLENFTSGSPFLCLMDLSYITALLKXGFGFADSTVLQ 400
DB 361 EVCNDLENFTSGSPFLCLMDLSYITALLKXGFGFADSTVLQ 400

RESULT 9
AAE19884
ID AAE19884 standard; protein; 465 AA.
XX
AC AAE19884;

XX DT 18-JUN-2002 (first entry)
XX DE Mouse CD39L4 protein.
XX KW Mouse; CD-39-like protein; CD39L4 protein; therapy; immune deficiency;
KW autoimmune disorder; multiple sclerosis; systemic lupus erythematosus;
KW rheumatoid arthritis; autoimmune thyroiditis; allergic reaction; asthma;
KW insulin dependent diabetes mellitus; periodontal disease; osteoporosis;
KW osteoarthritis; wound healing; tissue repair; Alzheimer's disease; ulcer;
KW Parkinson's disease; amyotrophic lateral sclerosis; Huntington's disease;
KW nervous system disease; nerve injury; ischaemia-reperfusion injury;
KW endotoxin lethality; arthritis; nephritis; inflammatory bowel disease;
KW Crohn's disease; viricide; antibacterial; antifungal; neuroprotective;
KW dermatological; immunosuppressive; vulnery; neurotropic; anticonvulsant;
KW antiinflammatory; nephrotropic; gastrointestinal; vasotropic; NTPase;
KW nucleotide-triphosphatase; enzyme.
XX OS Mus musculus.
XX US US6350447-B1.
XX PN 26-FEB-2002.
XX PD 29-JAN-1999; 99US-00240639.
XX PP 29-JAN-1999; 99US-00240639.
XX PR (HYSE-) HYSEQ INC.
XX PA Chadwick BP, Frieschaut A;
XX PI WPI: 2002-215262/27.
XX DR N-PSDB; AAD31696.
XX XX
XX PT An isolated polypeptide with phosphohydrolase activity, designated
XX PT CD39L2, useful to identify other proteins with which binding occurs or
XX PT identify inhibitors and for treatment of, e.g., Alzheimer's, multiple
XX PT sclerosis and osteoporosis.
XX PS Example; Fig 1; 101pp; English.
XX CC The present invention relates to novel proteins with phosphohydrolase
XX CC activity, designated CD-39-like (CD39L) proteins and polynucleotides
XX CC encoding such proteins. CD39L proteins are useful to treat infectious
XX CC diseases caused by viral, bacterial, fungal or other infection that may
XX CC be treatable with CD39L. They are useful in the treatment of various
XX CC immune deficiencies and disorders, autoimmune disorders such as multiple
XX CC sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune
XX CC thyroiditis and insulin dependent diabetes mellitus, allergic reactions
XX CC and conditions such as asthma and other respiratory problems, periodontal
XX CC disease, osteoporosis, osteoarthritis and other tooth repair processes.
XX CC They may have utility in compositions used for bone, cartilage, tendon,
XX CC ligament and/or nerve tissue growth or regeneration as well as for wound
XX CC healing and tissue repair and replacement and in the treatment of burns,
XX CC incisions and ulcers. CD39L proteins may also be useful for proliferation
XX CC of neural cells and for regeneration of nerve and brain tissue, i.e. for
XX CC the treatment of central nervous system diseases such as Alzheimer's
XX CC disease, Parkinson's disease, amyotrophic lateral sclerosis, Huntington's
XX CC disease, peripheral nervous system diseases peripheral nerve injuries,
XX CC peripheral neuropathy and localised neuropathies. They are also used to
XX CC treat mechanical and traumatic disorders which involve degeneration,
XX CC death or trauma to neural cells or nerve tissue. CD39L proteins of the
XX CC invention are also useful to promote better or faster closure of non-
XX CC healing wounds, including pressure ulcers, ulcers associated with
XX CC vascular insufficiency and surgical and traumatic wounds. They also
XX CC exhibit anti-inflammatory activity and may be used to treat inflammatory
XX CC conditions including chronic or acute conditions), including ischaemia-
XX CC reperfusion injury, endotoxin lethality, arthritis, nephritis, cytokine
XX CC or chemokine-induced lung injury, inflammatory bowel disease or Crohn's
XX CC disease. The present sequence is mouse CD39L4 protein, also known as
XX CC nucleotide-triphosphatase (NTPase)

XX PS Claim 11; Page 1429-1431; 2104pp; English.

XX CC AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53234 to AAB54006. The human colon cancer antigens can have cytostatic, cardioactive, muscular, neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnary, nephrotropic, antiinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polynucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polynucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, gastrointestinal disorders, muscular disorders, reproductive disorders, infectious diseases and disorders, wounds, renal disorders, infectious diseases and cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent sequences used in the exemplification of the present invention

XX SQ Sequence 330 AA;

Query Match 73.8%; Score 1660; DB 3; Length 330; Best Local Similarity 97.3%; Pred. No. 2.1e-151; Matches 319; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 101 AETVQGLLEVAKDSIPRSHWKTTPVVLKATAGLRLPEHKAALLFEVKGIFRKSPPFLVP 160

DB 3 ARAVQGLLEVAKDSIPRSHWKTTPVVLKATAGLRLPEHKAALLFEVKGIFRKSPPFLVP 62

QY 161 KGSVIMDGSDEGILAWTVNLTGQLHGHROSTVGTDLGGASTQTITLPOPEKLEQT 220

DB 63 KGSVIMDGSDEGILAWTVNLTGQLHGHROSTVGTDLGGASTQTITLPOPEKLEQT 122

QY 221 PRGLTSEFMFNSTYKLYTHSYLGFGLKAARLATGALTEGDTGHTFRSACLPRWLEAE 280

DB 123 PXGLTSEFMFNSTYKLYTHSYLGFGLKAARLATGALTEGDTGHTFRSACLPRWLEAE 182

QY 281 WIFGVKYQYQGNQGEVGPCEVAVLVRVGRKLHQPVEVQSGSFYAFSVYDRAVDT 340

DB 183 WIFGVKYQYQGNQGEVGPCEVAVLVRVGRKLHQPVEVQSGSFYAFSVYDRAVDT 242

QY 341 MIDYKGGILKVEDFERKAREVCDNLENFTSGSPFLCWLDSYITALLKDGFGFADSTVLQ 400

DB 243 MIDYKGGILKVEDFERKAREVCDNLENFTSGSPFLCWLDSYITALLKDGFGFADSTVLQ 302

QY 401 LTKVNNIETGVALGATFHLLQSLGISH 428

DB 303 LTKVNNIETGVALGATFHLLQSLGISH 330

RESULT 11

AAE19881 ID AAE19881 standard; protein; 456 AA.

XX AC AAE19881;

XX XX 18-JUN-2002 (first entry)

XX XX Human CD39L2 protein.

XX XX Human; CD-39-like protein; CD39L2 protein; therapy; immune deficiency; autoimmune disorder; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; autoimmune thyroiditis; allergic reaction; asthma; insulin dependent diabetes mellitus; periodontal disease; osteoporosis; osteoarthritis; wound healing; tissue repair; Alzheimer's disease; ulcer; Parkinson's disease; amyotrophic lateral sclerosis; Huntington's disease; nervous system disease; nerve injury; ischaemia-reperfusion injury; endotoxin lethality; arthritis; nephritis; inflammatory bowel disease; Crohn's disease; virucide; antibacterial; antifungal; neuroprotective; dermatological; immunosuppressive; vulnary; nephrotropic; anticonvulsant; antiinflammatory; nephrotropic; gastrointestinal; vasotropic.

XX OS Homo sapiens.

SQ Sequence 465 AA;

Query Match 81.4%; Score 1832.5; DB 5; Length 465; Best Local Similarity 83.8%; Pred. No. 7.9e-168; Matches 352; Conservative 25; Mismatches 40; Indels 3; Gaps 3;

QY 1 MATSGTVPFVNLVSCVSAVSHRNQQTWPEGIFLSSMCPINVSASTLYGIMFAGSTGT 60

DB 1 MATSGAV-FMLIIACVGTVPYRQQTWPEGVFLSSMCPINVSAGTFYGMFAGSTGA 59

QY 61 RIHVTFVQKMPGQLPILEGVFDVKFGLSAFVDQPKQAGTQVGLLEVAKDSIPRSHW 120

DB 60 RIHVTFVQKMPGQLPILEGVFDVKFGLSAFVDQPKQAGTQVGLLEVAKDSIPRSHW 119

QY 121 KKTVPVLKATAGLRLPEHKAALLFEVKGIFRKSPPFLVPKGSVIMDGSDEGILAWTV 180

DB 120 ERTVPVLKATAGLRLPEHKAALLFEVKGIFRKSPPFLVPKGSVIMDGSDEGILAWTV 179

QY 181 NPLTGQLHGHROSTVGTDLGGASTQTITLPOPEKLEQTTPRGYLTSEFMFNSTYKLYTH 240

DB 180 NPLTGQLHGHROSTVGTDLGGASTQTITLPOPEKLEQTTPRGYLTSEFMFNSTYKLYTH 239

QY 241 SYLGFGLKAARLATGALTEGDTGHTFRSACLPRWLEAEWIFGVKYQYQGNQGEVGP 300

DB 240 SYLGFGLKAARLATGALTEGDTGHTFRSACLPRWLEAEWIFGVKYQYQGNQGEVGP 299

QY 301 BPCYAEVLVRVGRKLHQPVEVQSGSFYAFSVYDRAVDTMIDYKGGILKVEDFERKAR 360

DB 300 BPCYAEVLVRVGRKLHQPVEVQSGSFYAFSVYDRAVDTMIDYKGGILKVEDFERKAR 359

QY 361 EYVDNLENFTSGSPFLCWLDSYITALLKDGFGFADSTVLQTLTKVNNIETGVALGATFHL 420

DB 360 EYVDNLENFTSGSPFLCWLDSYITALLKDGFGFADSTVLQTLTKVNNIETGVALGATFHL 417

RESULT 10

AAE53336 ID AAE53336 standard; protein; 330 AA.

XX AC AAE53336;

XX XX 09-MAR-2001 (first entry)

XX XX Human colon cancer antigen protein sequence SEQ ID NO:876.

XX XX Human; colon cancer; colon cancer antigen; diagnosis; detection; identification; cytostatic; cardioactive; neuroprotective; vulnary; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder.

XX OS Homo sapiens.

XX PN WO200055351-A1.

XX PD 21-SEP-2000.

XX PF 08-MAR-2000; 2000WO-US005883.

XX PR 12-MAR-1999; 99US-0124270P.

XX XX (HUMA-) HUMAN GENOME SCI INC.

XX XX Rosen CA, Ruben SM;

XX XX WPI; 2000-587534/55.

XX XX N-PSDE; AAC98033.

XX XX Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon disorders such as colon cancer.

XX US6350447-B1.
 XX 26-FEB-2002.
 XX 29-JAN-1999; 99US-00240639.
 XX 29-JAN-1999; 99US-00240639.
 XX (HYSE-) HYSEQ INC.
 XX Chadwick BP, Frischauf A;
 XX WPI: 2002-215262/27.
 XX N-PSDB; AAD31693.
 XX
 PT An isolated polypeptide with phosphohydrolase activity, designated
 PT CD39L2, useful to identify other proteins with which binding occurs or
 PT identify inhibitors and for treatment of, e.g., Alzheimer's, multiple
 PT sclerosis and osteoporosis.
 XX
 PS Claim 1; Fig 4; 101pp; English.
 XX
 CC The present invention relates to novel proteins with phosphohydrolase
 CC activity, designated CD-39-like (CD39L) proteins and polynucleotides
 CC encoding such proteins. CD39L proteins are useful to treat infectious
 CC diseases caused by viral, bacterial, fungal or other infection that may
 CC be treatable with CD39L. They are useful in the treatment of various
 CC immune deficiencies and disorders, autoimmune disorders such as multiple
 CC sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune
 CC thyroiditis and insulin dependent diabetes mellitus, allergic reactions
 CC and conditions such as asthma and other respiratory problems, periodontal
 CC disease, osteoporosis, osteoarthritis and other tooth repair processes.
 CC They may have utility in compositions used for bone, cartilage, tendon,
 CC ligament and/or nerve tissue growth or regeneration as well as for wound
 CC healing and tissue repair and replacement and in the treatment of burns,
 CC incisions and ulcers. CD39L proteins may also be useful for proliferation
 CC of neural cells and for regeneration of nerve and brain tissue, i.e. for
 CC the treatment of central nervous system diseases such as Alzheimer's
 CC disease, Parkinson's disease, amyotrophic lateral sclerosis, Huntington's
 CC disease, peripheral nervous system diseases peripheral nerve injuries,
 CC peripheral neuropathy and localised neuropathies. They are also used to
 CC treat mechanical and traumatic disorders which involve degeneration,
 CC death or trauma to neural cells or nerve tissue. CD39L proteins of the
 CC invention are also useful to promote better or faster closure of non-
 CC healing wounds, including pressure ulcers, ulcers associated with
 CC vascular insufficiency and surgical and traumatic wounds. They also
 CC exhibit anti-inflammatory activity and may be used to treat inflammatory
 CC conditions including chronic or acute conditions, including ischaemia-
 CC reperfusion injury, endotoxin lethality, arthritis, nephritis, cytokine
 CC or chemokine-induced lung injury, inflammatory bowel disease or Crohn's
 CC disease. The present sequence is human CD39L2 protein
 XX
 SQ Sequence 456 AA;
 Query March 44.4%; Score 999; DB 5; Length 456;
 Best Local Similarity 52.4%; Pred. No. 2.6e-87;
 Matches 204; Conservative 56; Mismatches 123; Indels 6; Gaps 4;
 QY 40 PINVSA---STLYGIMFDAGSTTRIRVYTFVQKMPGQILBEGVFDVSKPCLSAFVDQ 96
 DB 62 PLGTAGDGHGVYGVIMFDAGSTTRVHVFOFT-RPPRETPTLTHETFKAVKPLGSAYADD 120
 QY 97 PKQAGTVQGLLVKAVDSDIERSHWKTPVVLKATAGLLPEHKAALLPEVKEIPIKXGP 156
 DB 121 VESAGQIRELLSVAKQDIPDFWKAATPLVLKATAGLLPLGKAQLKQKVEFKASP 180
 QY 157 FLVPKGSVIMDSDEGILAWTVNFLTQGLHGHRETQVTLDLGASTQITPLPQFEKT 216
 DB 181 FLVGGDCCVSIIMNGTDEGVSAWITINFLTGLSKTPGGSSVGLDLGGSTQIAFLPRVEGT 240
 QY 217 LEQTPRGYLTSPFENSTYKLYTHSVGLGFLKKAARLATLGALETE-GTQGHTPRSACLPR 275

DB 241 LQASPPGYLTALRMFNFTYKLYSYSYGLGLMSARLAILGVGQOPAKDGHKELVSPCLSP 300
 QY 276 WLAEWIFGGYKYOYGNQGEVGFPCYAEVLVVRGKLHQPEEVQSGFYAFSYFYDR 335
 DB 301 SPKGEHAEVTVYRVSGKAAASLHELCAARVSEVLQNRVHRTTEEVKXVDFYAFSYFYDL 360
 QY 336 AVDTMDIDYERGGILKVEDFERKAREVDNLENTTSPPFLCMOLSVITALLKDGPGFAD 395
 DB 361 AAGVGLIDAERKGGSLVWGDFEIAAKYVCTLTETQPSPPSCMOLTVYVSLQLQ- FGPPR 419
 QY 396 STVQLTKKVNINIEGALGATFHLQSL 424
 DB 420 SKVLKTRKINDVETSWALGAIFHYIDSL 448

RESULT 12
 AAB72241
 ID AAB72241 standard; protein; 484 AA.
 AC AAB72241;
 XX
 DT 14-MAY-2001 (first entry)
 DE Human CD39 like protein CD39-L2 amino acid sequence.
 KW Human CD39-like protein; apyrase; NDPage; platelet function inhibitor;
 KW myocardial infarction; cerebral ischaemia; angina; arterial thrombosis;
 KW cerebral artery thrombosis; platelet aggregation; inflammation;
 KW apoptosis; autoimmune disorder; neurological disorder;
 KW Alzheimer's disease; Parkinson's disease; cancer; CD39-L2.
 OS Homo sapiens.
 XX WO200110205-A1.
 XX 15-FEB-2001.
 PR 09-AUG-2000; 2000WO-US021790.
 PR 09-AUG-1999; 99US-00370265.
 PR 11-JAN-2000; 2000US-00481238.
 PR 25-APR-2000; 2000US-00557800.
 PR 26-MAY-2000; 2000US-00583231.
 PR 30-JUN-2000; 2000US-00608285.
 XX (HYSE-) HYSEQ INC.
 PI Ford J, Mulero JJ, Yeung G;
 DR WPI; 2001-147489/15.
 DR N-PSDB; AAP63386.
 PT Polynucleotides encoding human CD39-like polypeptides, with apyrase
 PT and/or NDPage activity, which are useful in the treatment of pathological
 PT conditions caused by thrombosis (e.g. myocardial infarction) and
 PT inflammatory disorders.
 XX Claim 39; Page 162-164; 203pp; English.

XX This invention relates to polynucleotides encoding human CD39-like
 CC polypeptides with apyrase and/or NDPage activity. The polypeptides having
 CC apyrase, including NDPage, activity are useful for inhibiting platelet
 CC function and can therefore be used in the prophylaxis or treatment of
 CC pathological conditions caused by or involving thrombosis or excessive
 CC coagulation or excessive platelet aggregation, such as myocardial
 CC infarction, cerebral ischaemia, angina, arterial thrombosis, associated
 CC artery thrombosis or intracardiac thrombosis, and conditions associated
 CC with venous thrombosis. CD39-L4 and CD39-L2 polypeptides are useful in
 CC modulating disease states (including platelet aggregation, inflammation
 CC and apoptosis) associated with ADP or other purinergic signalling by
 CC reducing the levels of NDPS. The polypeptides are also useful for
 CC prophylaxis or treatment of inflammation related disorders, such as
 CC disorders involving sepsis or systemic inflammatory response syndrome or

Db 427 SKVLKTRKIDNVETSWALGAIPIFYIDSL 455

RESULT 14

ABJ04657

ID ABJ04657 standard; protein; 467 AA.

XX AC ABJ04657;

XX DT 11-OCT-2002 (first entry)

XX DE Protein of NOVX 15a SEQ ID No 36.

XX KW Cytostatic; antidiabetic; anorectic; metabolic; nootropic; antilipaeamic;

XX KW neuroprotective; antiparkinsonian; anticonvulsant; cerebroprotective;

XX KW tranquiliser; neuroleptic; antidiabetic; antitumor; antiinflammatory;

XX KW anti-HIV; antiallergic; antirheumatic; antiarthritic; NOVX; diabetes;

XX KW metabolic disorder; obesity; infectious diseases; Alzheimer's disease;

XX KW anorexia; neurodegenerative disorder; Parkinson's disorder; obesity;

XX KW immune disorder; haematopoietic disorder; dyslipidaemia; chronic disease;

XX KW metabolic syndrome X; wasting disorder; cancer; neurological disorder;

XX KW epilepsy; stroke; mental disorder; schizophrenia; goiter;

XX KW vesicular transport; cystic fibrosis; gastrointestinal disorder;

XX KW diabetes mellitus; ulcerative colitis; AIDS; allergic reaction;

XX KW multiple sclerosis; rheumatoid arthritis; transgenic animal;

XX KW gene therapy.

XX OS Unidentified.

XX PN W0200246409-A2.

XX 13-JUN-2002.

XX 06-DEC-2001; 2001WO-US046586.

XX 06-DEC-2000; 2000US-02516602.

XX 12-DEC-2000; 2000US-0255029P.

XX 08-JAN-2001; 2001US-0260346P.

XX 24-JAN-2001; 2001US-0263800P.

XX 20-FEB-2001; 2001US-0269942P.

XX 24-APR-2001; 2001US-0286183P.

XX 20-AUG-2001; 2001US-0313627P.

XX 12-SEP-2001; 2001US-0318712P.

XX (CURA-) CURAGEN CORP.

XX Guo X, Li L, Patturajan M, Shankets RA, Casman SJ, Malyankar UM;

XX Tchernev VT, Vernet CAM, Spytek KA, Shency SG, Alsobrook JP;

XX Edinger S, Peyman JA, Stone DJ, Ellerman K, Gangolli EA, Boldog FL;

XX Colman SD, Eison AJ, Liu X, Padigaru M, Spaderna SK, Zerhusen BD;

XX WPI; 2002-547774/58.

XX N-PSDB; AET05470.

XX Novel isolated polypeptide, designated NOVX, useful for treating or

XX preventing cancer, diabetes, obesity, dyslipidemia, anorexia, and

XX metabolic, neurodegenerative, immune and hematopoietic disorders.

XX Claim 1; Page 140; 421pp; English.

XX The invention relates to an isolated polypeptide, designated NOVX,

XX comprising a sequence fully defined in the specification. The isolated

XX protein, its encoding polynucleotide or an antibody created from the

XX protein is useful in the manufacture of a medicament for treating a

XX syndrome associated with a human disease, preferably a NOVX-associated

XX disorder, or for treating or preventing a NOVX-associated disorder in a

XX subject, preferably human. The isolated protein, its encoding

XX polynucleotide or an antibody created from the protein are also useful

XX for treating or preventing metabolic disorders, diabetes, obesity,

XX infectious disease, anorexia, neurodegenerative disorder, Alzheimer's

XX disease, Parkinson's disorder, immune disorders, haematopoietic

XX disorders, and various dyslipidaemias, metabolic disturbances associated

XX with obesity, the metabolic syndrome X, wasting disorders associated with

CC chronic diseases, and cancer. The isolated protein, its encoding

CC polynucleotide or an antibody created from the protein are useful for

CC treating or preventing neurological disorders such as epilepsy, stroke,

CC mental disorders including mood, anxiety, schizophrenic disorders,

CC disorders of vesicular transport such as cystic fibrosis, diabetes

CC mellitus, goiter, gastrointestinal disorders including ulcerative

CC colitis, other conditions associated with abnormal vesicle trafficking

CC including AIDS, allergic reactions, multiple sclerosis and rheumatoid

CC arthritis. A cell comprising the vector of the invention is useful for

CC producing non-human transgenic animals. The polynucleotide of the

CC invention can be used to treat disorders by gene therapy. This sequence

CC represents one of the isolated NOVX proteins of the invention

XX

XX Sequence 467 AA;

XX Query Match 44.3%; Score 996; DB 5; Length 467;

XX Best Local Similarity 52.2%; Pred. No. 5.2e-87;

XX Matches 203; Conservative 57; Mismatches 123; Indels 6; Gaps 4;

QY 40 PINVA---STLYGIMFDAGSTGTRHVVTFVQKMPGOLPILGEVEDSVKPLSAFVDQ 96

DB 73 PLGTAAAGHEVTFYGMFDAGSTGTRHVVFPQFT-REPRTPTLTHTFKALKPLSAYADD 131

QY 97 PRQGAETVQGLLEVARQDSIPRSHWKTTPVVLKATAGLRLPHHAKALLFEVKEIFRKSP 156

DB 132 VEKSAGGIRELLDVAQDIPDFWKATPLVLKATAGLRLPHHAKALLFEVKEIFRKSP 191

QY 157 FLVPKGSVIMDSDEGILLANVTNLTQGLHGRQETVGTLDLGGCASTQITLPOPEKT 216

DB 192 FLVGDDCVSINGTDEGVSAMITINFLTGSLTKTPGSSVGMDDGGSTQIAELPRVEGT 251

QY 217 LEOTPRGYLTSPFEMFNSTYKLYTHSYLGFGLKAARLATIAGALETE-GTIDHTFRSACLPR 275

DB 252 LQASPPGYLTALPMFRTYKLYSYLGLGASARLAILGGVGPQAKDKELVSPCLSP 311

QY 276 WLEAEMIFGCVKYQYCGNORGEVGFPCYAEVLVRVGRKLGHOPEKVGQSGFYAFSYDYR 335

DB 312 SPKGEWEHAEVTVRVSGQKAASLHELCAARVSEVLQNRVHRTVEVGVDFYAFSYDYDL 371

QY 336 AVTDMIDYKGGIILKVEDFERKAREVCNLENTSGSPFLCMDSLVIITALLKDGFGFAD 395

DB 372 AAGVGUIDAEKGSLSLVGDFEIAAKVVCRTLETPQSSPSCMDLTVVSLLLQE-FGFP 430

QY 396 STYQLTKKYNNTETGALGATFHLQSL 424

DB 431 SKVLKTRKIDNVETSWALGAIPIFYIDSL 459

RESULT 15

AAW93929

ID AAW93929 standard; protein; 456 AA.

XX AC AAW93929;

XX DT 06-NOV-2001 (first entry)

XX DE Human polypeptide, SEQ ID NO: 4100.

XX KW Human; full length cDNA; cDNA synthesis; oligo-capping.

XX OS Homo sapiens.

XX FN EP1130094-A2.

XX PD 05-SEP-2001.

XX PF 07-JUL-2000; 2000EP-00114089.

XX PR 08-JUL-1999; 99JP-00194486.

XX PR 11-JAN-2000; 2000JP-00118774.

XX PR 02-MAY-2000; 2000JP-00183765.

XX (HELI-) HELIX RES INST.

[illegible]

Search completed: July 1, 2004, 13:46:36
Job time : 54 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 1, 2004, 13:48:47 ; Search time 44.5 Seconds
(without alignments)
2993.921 Million cell updates/sec

Title: US-10-091-085-3
Perfect score: 2250
Sequence: 1 MATSGTGFVFLVSCVCSA.....ETGVALGATFHLQSLGISH 428

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues 1276540
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
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2: /cgn2_6/prodata/1/pubpaa/US07_PUB_PUB.pep.*
3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep.*
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16: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2250	100.0	428	13	US-10-091-085-3
2	2250	100.0	428	13	US-10-091-085-5
3	2250	100.0	428	13	US-10-092-063-3
4	2250	100.0	428	13	US-10-092-063-5
5	2250	100.0	428	14	US-10-286-926-3
6	2250	100.0	428	15	US-10-286-926-5
7	2250	100.0	428	15	US-10-231-913-127
8	2236	99.4	428	16	US-10-408-765A-2296
9	2235	99.3	428	13	US-10-091-085-7
10	2235	99.3	428	13	US-10-092-063-7
11	2235	99.3	428	14	US-10-286-926-7
12	2104	93.5	405	13	US-10-092-063-25
13	2104	93.5	405	14	US-10-286-926-25
14	1994.5	88.6	427	15	US-10-231-913-126
15	1837.5	81.7	465	13	US-10-092-063-39

16	1660	73.8	330	9	US-09-925-299-876	Sequence 876, App
17	1660	73.8	330	10	US-09-925-299-876	Sequence 876, App
18	999	44.4	484	13	US-10-092-063-27	Sequence 27, Appl
19	999	44.4	484	14	US-10-286-926-27	Sequence 27, Appl
20	999	44.4	484	15	US-10-231-913-123	Sequence 123, Appl
21	996	44.3	467	15	US-10-231-913-36	Sequence 36, Appl
22	993.5	44.2	379	15	US-10-231-913-271	Sequence 124, Appl
23	992	44.1	484	15	US-10-231-913-124	Sequence 271, Appl
24	989	44.0	446	15	US-10-231-913-38	Sequence 38, Appl
25	986	43.8	455	15	US-10-231-913-125	Sequence 125, Appl
26	616.5	27.4	479	15	US-10-369-493-6447	Sequence 6447, Ap
27	590	26.2	476	9	US-09-835-147-4	Sequence 4, Appl
28	538.5	23.9	556	15	US-10-369-493-2169	Sequence 2169, Ap
29	533	23.7	476	9	US-09-835-147-3	Sequence 3, Appl
30	507.5	22.6	459	9	US-09-129-112-9	Sequence 9, Appl
31	503.5	22.4	467	9	US-09-129-112-19	Sequence 19, Appl
32	503	22.4	410	15	US-10-231-913-272	Sequence 272, App
33	503	22.4	467	12	US-10-425-114-45875	Sequence 45875, A
34	498	22.1	462	9	US-09-139-112-2	Sequence 2, Appl
35	498	22.1	534	16	US-10-437-963-132351	Sequence 132351,
36	491.5	21.8	462	9	US-09-129-112-15	Sequence 15, Appl
37	491	21.8	433	12	US-10-425-114-36762	Sequence 36762, A
38	490	21.8	467	12	US-10-424-599-230158	Sequence 230158,
39	483.5	21.5	518	15	US-10-369-493-1713	Sequence 1713, Ap
40	474.5	21.1	443	12	US-10-425-114-49933	Sequence 49933, A
41	459.5	20.4	457	12	US-10-425-114-51762	Sequence 51762, A
42	459.5	20.4	459	12	US-10-424-599-145076	Sequence 145076,
43	455.5	20.2	472	16	US-10-437-963-151710	Sequence 151710,
44	445.5	19.8	465	12	US-10-425-114-37241	Sequence 37241, A
45	445.5	19.8	465	12	US-10-425-114-49932	Sequence 49932, A

ALIGNMENTS

RESULT 1

US-10-091-085-3
; Sequence 3, Application US/10091085
; Publication No. US2002014672A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; FILE REFERENCE: 28110/35761
; CURRENT APPLICATION NUMBER: US/10/091,085
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-091-085-3

Query Match 100.0%; Score 2250; DB 13; Length 428;
Best Local Similarity 100.0%; Pred. NO. 5.6e-215;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MATSGTGFVFLVSCVCSAVSHRNOQTWFEGIFLSSMCPINVSASTLYGINFDAQSTGT 60
1 MATSGTGFVFLVSCVCSAVSHRNOQTWFEGIFLSSMCPINVSASTLYGINFDAQSTGT 60

QY 61 RIHYVTFVQKMPQGLPILGEVFDVSKPGLSAFVDPQKGAETVQGLLEVAKDSIPRSHW 120
 DB 61 RIHYVTFVQKMPQGLPILGEVFDVSKPGLSAFVDPQKGAETVQGLLEVAKDSIPRSHW 120
 QY 121 KKTPTVVLKATAGLRLLPEHKAKALLFEVKEIFRKSPPFLVPKGSVIMDGSDEGILAWTV 180
 DB 121 KKTPTVVLKATAGLRLLPEHKAKALLFEVKEIFRKSPPFLVPKGSVIMDGSDEGILAWTV 180
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 QY 241 SYLGFGGLKAARLALATLGALETGTGHTFRSACLPRWLEAEWIFGGVKKYQYGGNQGEGVGF 300
 DB 241 SYLGFGGLKAARLALATLGALETGTGHTFRSACLPRWLEAEWIFGGVKKYQYGGNQGEGVGF 300
 QY 301 EPCYAEVLRVVRGKLHQPVEVQSGFYAFSYYYDRAVDTMDIDYKGGILKVEDPERKAR 360
 DB 301 EPCYAEVLRVVRGKLHQPVEVQSGFYAFSYYYDRAVDTMDIDYKGGILKVEDPERKAR 360
 QY 361 EVCNLENTSSGPFCLMDLSYITALLKDGFGFADSTVLQLTKKVNNIETGVALGATPHL 420
 DB 361 EVCNLENTSSGPFCLMDLSYITALLKDGFGFADSTVLQLTKKVNNIETGVALGATPHL 420
 QY 421 LQSLGISH 428
 DB 421 LQSLGISH 428

RESULT 2

US-10-091-085-5
 ; Sequence 5, Application US/10091085
 ; Publication No. US20020146772A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ford, John
 ; APPLICANT: Mulero, Julio
 ; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
 ; FILE REFERENCE: 28110/35761
 ; CURRENT APPLICATION NUMBER: US/10/091,085
 ; CURRENT FILING DATE: 2002-03-05
 ; PRIOR APPLICATION NUMBER: 09/350,836
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: 09/273,447
 ; PRIOR FILING DATE: 1999-03-19
 ; PRIOR APPLICATION NUMBER: 09/118,205
 ; PRIOR FILING DATE: 1998-07-16
 ; PRIOR APPLICATION NUMBER: 09/122,449
 ; PRIOR FILING DATE: 1998-07-24
 ; PRIOR APPLICATION NUMBER: 09/244,444
 ; PRIOR FILING DATE: 1999-02-04
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 428
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-091-085-5

Query Match 100.0%; Score 2250; DB 13; Length 428;
 Best Local Similarity 100.0%; Pred. No. 5.6e-215;
 Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATSNGTVPFMLVVCVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
 DB 1 MATSNGTVPFMLVVCVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
 QY 61 RIHYVTFVQKMPQGLPILGEVFDVSKPGLSAFVDPQKGAETVQGLLEVAKDSIPRSHW 120
 DB 61 RIHYVTFVQKMPQGLPILGEVFDVSKPGLSAFVDPQKGAETVQGLLEVAKDSIPRSHW 120
 QY 121 KKTPTVVLKATAGLRLLPEHKAKALLFEVKEIFRKSPPFLVPKGSVIMDGSDEGILAWTV 180

DB 121 KKTPTVVLKATAGLRLLPEHKAKALLFEVKEIFRKSPPFLVPKGSVIMDGSDEGILAWTV 180
 QY 181 NFLTGQLHGHROETVGTDLGGASTQITFLPQPEKTLQTPRGYLTSEMFNSTYKLYTH 240
 DB 181 NFLTGQLHGHROETVGTDLGGASTQITFLPQPEKTLQTPRGYLTSEMFNSTYKLYTH 240
 QY 241 SYLGFGGLKAARLALATLGALETGTGHTFRSACLPRWLEAEWIFGGVKKYQYGGNQGEGVGF 300
 DB 241 SYLGFGGLKAARLALATLGALETGTGHTFRSACLPRWLEAEWIFGGVKKYQYGGNQGEGVGF 300
 QY 301 EPCYAEVLRVVRGKLHQPVEVQSGFYAFSYYYDRAVDTMDIDYKGGILKVEDPERKAR 360
 DB 301 EPCYAEVLRVVRGKLHQPVEVQSGFYAFSYYYDRAVDTMDIDYKGGILKVEDPERKAR 360
 QY 361 EVCNLENTSSGPFCLMDLSYITALLKDGFGFADSTVLQLTKKVNNIETGVALGATPHL 420
 DB 361 EVCNLENTSSGPFCLMDLSYITALLKDGFGFADSTVLQLTKKVNNIETGVALGATPHL 420
 QY 421 LQSLGISH 428
 DB 421 LQSLGISH 428

RESULT 3

US-10-092-063-3
 ; Sequence 3, Application US/10092063
 ; Publication No. US20020173005A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ford, John
 ; APPLICANT: Mulero, Julio
 ; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDE
 ; FILE REFERENCE: 28110/35908
 ; CURRENT APPLICATION NUMBER: US/10/092,063
 ; CURRENT FILING DATE: 2002-03-05
 ; PRIOR APPLICATION NUMBER: 09/370,265
 ; PRIOR FILING DATE: 2002-01-31
 ; PRIOR APPLICATION NUMBER: PCT/US99/16180
 ; PRIOR FILING DATE: 1999-07-16
 ; PRIOR APPLICATION NUMBER: 09/350,836
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: 09/273,447
 ; PRIOR FILING DATE: 1999-03-19
 ; PRIOR APPLICATION NUMBER: 09/244,444
 ; PRIOR FILING DATE: 1999-02-04
 ; PRIOR APPLICATION NUMBER: 09/122,449
 ; PRIOR FILING DATE: 1998-07-24
 ; PRIOR APPLICATION NUMBER: 09/118,205
 ; PRIOR FILING DATE: 1998-07-16
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 428
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-092-063-3

Query Match 100.0%; Score 2250; DB 13; Length 428;
 Best Local Similarity 100.0%; Pred. No. 5.6e-215;
 Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MATSNGTVPFMLVVCVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
 DB 1 MATSNGTVPFMLVVCVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
 QY 61 RIHYVTFVQKMPQGLPILGEVFDVSKPGLSAFVDPQKGAETVQGLLEVAKDSIPRSHW 120
 DB 61 RIHYVTFVQKMPQGLPILGEVFDVSKPGLSAFVDPQKGAETVQGLLEVAKDSIPRSHW 120
 QY 121 KKTPTVVLKATAGLRLLPEHKAKALLFEVKEIFRKSPPFLVPKGSVIMDGSDEGILAWTV 180
 DB 121 KKTPTVVLKATAGLRLLPEHKAKALLFEVKEIFRKSPPFLVPKGSVIMDGSDEGILAWTV 180
 QY 181 NFLTGQLHGHROETVGTDLGGASTQITFLPQPEKTLQTPRGYLTSEMFNSTYKLYTH 240

Db 181 NLTGQLHGHROETVGTLDLGASTQITFLPQFTEKLEQTPRGYLTSFEMFNSTYKLYTH 240
Qy 241 SYLGFGLKAARLALATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYCGNQEYVGF 300
Db 241 SYLGFGLKAARLALATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYCGNQEYVGF 300
Qy 301 EPCYAEVLVRVGRKHLQHPQEVQSGFYAFSYYYDRAVDMDIDYKGGILKVEDPERKAR 360
Db 301 EPCYAEVLVRVGRKHLQHPQEVQSGFYAFSYYYDRAVDMDIDYKGGILKVEDPERKAR 360
Qy 361 EYCDNLENFTSGSPFLCMLDLSYITALLKDGFGFADSTVLQTLTKKNNIETGHALGATPHL 420
Db 361 EYCDNLENFTSGSPFLCMLDLSYITALLKDGFGFADSTVLQTLTKKNNIETGHALGATPHL 420
Qy 421 LQSLGISH 428
Db 421 LQSLGISH 428

RESULT 4
US-10-092-063-5
; Sequence 5, Application US/10092063
; Publication No. US20020173005A1
; GENERAL INFORMATION:
; APPLICANT: Mulero, Julio
; APPLICANT: Ford, John
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
; FILE REFERENCE: 28110/35908
; CURRENT APPLICATION NUMBER: US/10/092,063
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-063-5

Query Match 100.0%; Score 2250; DB 13; Length 428;
Best Local Similarity 100.0%; Pred. No. 5.6e-215;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MATSWGTVFFMLVAVSCVSAVSHRNQQTWFEIGFLSSMCPINVSASTLYGIMFDAGSTGT 60
Db 1 MATSWGTVFFMLVAVSCVSAVSHRNQQTWFEIGFLSSMCPINVSASTLYGIMFDAGSTGT 60
Qy 61 RIHVYTFVQKMPGQLPILEGVFDVSXKPLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
Db 61 RIHVYTFVQKMPGQLPILEGVFDVSXKPLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
Qy 121 KCTPVLKATAGLLPEHAKALLFEVKIEPRKSPFLVPKGSVIMDGSDEGILLAWTV 180
Db 121 KCTPVLKATAGLLPEHAKALLFEVKIEPRKSPFLVPKGSVIMDGSDEGILLAWTV 180
Qy 181 NLTGQLHGHROETVGTLDLGASTQITFLPQFTEKLEQTPRGYLTSFEMFNSTYKLYTH 240
Db 181 NLTGQLHGHROETVGTLDLGASTQITFLPQFTEKLEQTPRGYLTSFEMFNSTYKLYTH 240

Qy 241 SYLGFGLKAARLALATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYCGNQEYVGF 300
Db 241 SYLGFGLKAARLALATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYCGNQEYVGF 300
Qy 301 EPCYAEVLVRVGRKHLQHPQEVQSGFYAFSYYYDRAVDMDIDYKGGILKVEDPERKAR 360
Db 301 EPCYAEVLVRVGRKHLQHPQEVQSGFYAFSYYYDRAVDMDIDYKGGILKVEDPERKAR 360
Qy 361 EYCDNLENFTSGSPFLCMLDLSYITALLKDGFGFADSTVLQTLTKKNNIETGHALGATPHL 420
Db 361 EYCDNLENFTSGSPFLCMLDLSYITALLKDGFGFADSTVLQTLTKKNNIETGHALGATPHL 420
Qy 421 LQSLGISH 428
Db 421 LQSLGISH 428

RESULT 5
US-10-286-926-3
; Sequence 3, Application US/10286926
; Publication No. US20030175752A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; FILE REFERENCE: 28110/36457CON
; CURRENT APPLICATION NUMBER: US/10/286,926
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-926-3

Query Match 100.0%; Score 2250; DB 14; Length 428;
Best Local Similarity 100.0%; Pred. No. 5.6e-215;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MATSWGTVFFMLVAVSCVSAVSHRNQQTWFEIGFLSSMCPINVSASTLYGIMFDAGSTGT 60
Db 1 MATSWGTVFFMLVAVSCVSAVSHRNQQTWFEIGFLSSMCPINVSASTLYGIMFDAGSTGT 60
Qy 61 RIHVYTFVQKMPGQLPILEGVFDVSXKPLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
Db 61 RIHVYTFVQKMPGQLPILEGVFDVSXKPLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
Qy 121 KCTPVLKATAGLLPEHAKALLFEVKIEPRKSPFLVPKGSVIMDGSDEGILLAWTV 180
Db 121 KCTPVLKATAGLLPEHAKALLFEVKIEPRKSPFLVPKGSVIMDGSDEGILLAWTV 180
Qy 181 NLTGQLHGHROETVGTLDLGASTQITFLPQFTEKLEQTPRGYLTSFEMFNSTYKLYTH 240

Db 191 NLTGQLHGRQETVGTLDLGGASTQITFLPQFKTELEQTPRGYLTSPFENSTYKLYTH 240
Qy 241 SYLAFGLKAARLATLGALETEGDTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEVGF 300
Db 241 SYLAFGLKAARLATLGALETEGDTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEVGF 300
Qy 301 EPCYAEVLVRVGRKLGHPBEVQSGFYAFSYYYDRAVDMDIDYKGGILKVEDPFRKAR 360
Db 301 EPCYAEVLVRVGRKLGHPBEVQSGFYAFSYYYDRAVDMDIDYKGGILKVEDPFRKAR 360
Qy 361 EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQLTCKVNNIETGVALGATFHL 420
Db 361 EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQLTCKVNNIETGVALGATFHL 420
Qy 421 LQSLGISH 428
Db 421 LQSLGISH 428

RESULT 6

US-10-286-926-5
; Sequence 5, Application US/10286926
; Publication No. US20030175752A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 28110/36457CON
; CURRENT APPLICATION NUMBER: US/10/286,926
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-926-5

Query Match 100.0%; Score 2250; DB 14; Length 428;
Best Local Similarity 100.0%; Pred. No. 5.6e-215;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MATSGNTVFVFLVSCVSAVSHRNQQTWFERGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
Db 1 MATSGNTVFVFLVSCVSAVSHRNQQTWFERGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
Qy 61 RIHYVTFVQKMPGQLPILLEGVFDVSKPGLSAFVDQPKQGAETVQGLLEAKDSIPRSHW 120
Db 61 RIHYVTFVQKMPGQLPILLEGVFDVSKPGLSAFVDQPKQGAETVQGLLEAKDSIPRSHW 120
Qy 121 KKTVPVLKATAGLLELPEHKAKALLFEVKEIFRKSPLVPKGSVINDSGDEGLAWTV 180

Db 121 KKTVPVLKATAGLLELPEHKAKALLFEVKEIFRKSPLVPKGSVINDSGDEGLAWTV 180
Qy 181 NLTGQLHGRQETVGTLDLGGASTQITFLPQFKTELEQTPRGYLTSPFENSTYKLYTH 240
Db 181 NLTGQLHGRQETVGTLDLGGASTQITFLPQFKTELEQTPRGYLTSPFENSTYKLYTH 240
Qy 241 SYLAFGLKAARLATLGALETEGDTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEVGF 300
Db 241 SYLAFGLKAARLATLGALETEGDTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEVGF 300
Qy 301 EPCYAEVLVRVGRKLGHPBEVQSGFYAFSYYYDRAVDMDIDYKGGILKVEDPFRKAR 360
Db 301 EPCYAEVLVRVGRKLGHPBEVQSGFYAFSYYYDRAVDMDIDYKGGILKVEDPFRKAR 360
Qy 361 EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQLTCKVNNIETGVALGATFHL 420
Db 361 EVCNLENFTSGSPFLCMLDSYITALLKDGFGFADSTVLQLTCKVNNIETGVALGATFHL 420
Qy 421 LQSLGISH 428
Db 421 LQSLGISH 428

RESULT 7

US-10-231-913-127
; Sequence 127, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia S.
; APPLICANT: Li, Li
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Edinger, Schlomit
; APPLICANT: Peyman, John A.
; APPLICANT: Stone, David J.
; APPLICANT: Gangolli, Beha A.
; APPLICANT: Boldog, Ference L.
; APPLICANT: Colman, Steven D.
; APPLICANT: Eisen, Andrew J.
; APPLICANT: Liu, Xiachong
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-216
; CURRENT APPLICATION NUMBER: US/10/231,913
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/251,660
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/255,029
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/260,326
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/263,800
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/269,942
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/286,183
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/313,627
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/318,712
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 127
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-231-913-127

Query Match      100.0%; Score 2250; DB 15; Length 428;
Best Local Similarity 100.0%; Pred. No. 5.6e-215;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATSWGTVFFMLVWSCVCSAVSHRNOQTWFEGLFLLSSMCPINVSASTLYGIMFDAGSTGT 60
DB |||||
QY 61 RIHVYTFVQKMPGQLPILGEVFDVSKPGLSAFVDPKQGAETVQGLLEVAKDSIPRSHW 120
DB |||||
QY 61 RIHVYTFVQKMPGQLPILGEVFDVSKPGLSAFVDPKQGAETVQGLLEVAKDSIPRSHW 120
DB |||||
QY 121 KXTPVVLKATAGLRLLPEHKAALLFEVKIIFRKSPLVPKGSVIMDGSDEGILAWTV 180
DB |||||
QY 181 NFLTQGLHGRQETVTGLDGGASTQITFLPQFEKTLQTPRGYLTSEFNFSTYKLYTH 240
DB |||||
QY 181 NFLTQGLHGRQETVTGLDGGASTQITFLPQFEKTLQTPRGYLTSEFNFSTYKLYTH 240
DB |||||
QY 241 SYLGFGLKAARLALATLGALETEGTDGHTFRSACLPRWLEAEWIFGGVKIYQYGGNQEVEGF 300
DB |||||
QY 301 EPCYAEVLVRVGRKGLHQPVEVQSGFYAFSYVDRAVDTMDIDYEKGGILKVEDFERKAR 360
DB |||||
QY 301 EPCYAEVLVRVGRKGLHQPVEVQSGFYAFSYVDRAVDTMDIDYEKGGILKVEDFERKAR 360
DB |||||
QY 361 EVCNLENFTSGSPFLCWDLSYITALLKDGFGFADSTVLQLTKKVNNIETGVALGATFHL 420
DB |||||
QY 421 LQSLGISH 428
DB |||||
QY 421 LQSLGISH 428
DB |||||

RESULT 9
US-10-091-085-7
; Sequence 7, Application US/10091085
; Publication No. US20020146772A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/35761
; CURRENT APPLICATION NUMBER: US/10/091,085
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-091-085-7

Query Match      99.3%; Score 2235; DB 13; Length 428;
Best Local Similarity 99.3%; Pred. No. 1.7e-213;
Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MATSWGTVFFMLVWSCVCSAVSHRNOQTWFEGLFLLSSMCPINVSASTLYGIMFDAGSTGT 60
DB |||||
QY 61 RIHVYTFVQKMPGQLPILGEVFDVSKPGLSAFVDPKQGAETVQGLLEVAKDSIPRSHW 120
DB |||||
QY 61 RIHVYTFVQKMPGQLPILGEVFDVSKPGLSAFVDPKQGAETVQGLLEVAKDSIPRSHW 120
DB |||||

RESULT 8
US-10-408-765A-2296
; Sequence 2296, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2296
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-408-765A-2296

Query Match      99.4%; Score 2236; DB 16; Length 428;
Best Local Similarity 99.5%; Pred. No. 1.4e-213;
Matches 426; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATSWGTVFFMLVWSCVCSAVSHRNOQTWFEGLFLLSSMCPINVSASTLYGIMFDAGSTGT 60
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QY	121	KKT	PVVLKATAGRLRLLPEHKAKALLFEVKBI	FRKSPFLVPKGVSIMDGSDEGILLAWTV	180
Db	121	KKT	PVVLKATAGRLRLLPEHKAKALLFEVKBI	FRKSPFLVPKGVSIMTQDSGFANWTV	180
QY	181	NFLTQLGHGRQETVGTLLDLGGASTQTIFP	POPEKTELEOTPRGYLTSFEMFNSTYKLXTH	240	
Db	181	NFLTQLGHGRQETVGTLLDLGGASTQTIFP	POPEKTELEOTPRGYLTSFEMFNSTYKLXTH	240	
QY	241	SVLFGPLKAARLATI	GALLETSGTDTGHTFRSACLPWLAEAEWI	FGGVKYQYGCNQGEVGCF	300
Db	241	SVLFGPLKAARLATI	GALLETSGTDTGHTFRSACLPWLAEAEWI	FGGVKYQYGCNQGEVGCF	300
QY	301	EPCYAELVRVRGKHQEPVEEVQRGSFYAFSY	YYDRAVDTMDMIYEYKGGILKVEDPERKAR	360	
Db	301	EPCYAELVRVRGKHQEPVEEVQRGSFYAFSY	YYDRAVDTMDMIYEYKGGILKVEDPERKAR	360	
QY	361	EVCNDLENFTSGSPFLCNDLSVIITALLKDGF	PADSTVLQLTKKVNNIETGWALGATFHLL	420	
Db	361	EVCNDLENFTSGSPFLCNDLSVIITALLKDGF	PADSTVLQLTKKVNNIETGWALGATFHLL	420	
QY	421	LQSLGISH	428		
Db	421	LQSLGISH	428		

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RESULT 10
US-10-092-063-7
; Sequence 7, Application US/10092063
; Publication No. US2002173005A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Muletto, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
; FILE REFERENCE: 28110/35908
; CURRENT APPLICATION NUMBER: US/10/092,063
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 7
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
; 10-092-063-7

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Db	121	KKT	PVVLKATAGLRLLPEHKAKALLPEVFKBI	FRKSPFLVPKGSVSNMTQDEGIFAWTV	180
Qy	181	NFLT	QGLHGHROETVGTDLGGASTQITLPPQFKTELEQTPRGYLTSFEMFNSTYKLYTH	240	
Db	181	NFLT	QGLHGHROETVGTDLGGASTQITLPPQFKTELEQTPRGYLTSFEMFNSTYKLYTH	240	
Qy	241	SYL	FGGLKAARLATLGALETEGTDGHTFSSACLPRLWEAEWIFGGVKYQYGGNQBEVGVF	300	
Db	241	SYL	FGGLKAARLATLGALETEGTDGHTFSSACLPRLWEAEWIFGGVKYQYGGNQBEVGVF	300	
Qy	301	EP	CYAEVLRVVRKGLQPEEVQRGSTFAPSYYYVDRAVDTMDIMDYBKGGILKVBDFPERKAR	360	
Db	301	EP	CYAEVLRVVRKGLHOPBEVQRGSTFAPSYYYVDRAVDTMDIMDYBKGGILKVBDFPERKAR	360	
Qy	361	EVC	DNLENFTSGSPFLCMDSLVIYITALLKDGFGPADSTVLQLTKKVNNIETGWAIGATFHL	420	
Db	361	EVC	DNLENFTSGSPFLCMDSLVIYITALLKDGFGPADSTVLQLTKKVNNIETGWAIGATFHL	420	
Qy	421	LOS	LIGISH	428	
Db	421	LOS	LIGISH	428	

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RESULT 11
US-10-286-926-7
; Sequence 7, Application US/10286926
; Publication No. US20030175752A1
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 28110/36457CON
; CURRENT APPLICATION NUMBER: US/10/286,926
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-926-7

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Query Match	99.3%	Score 2235;	DB 14;	Length 428;
Best Local Similarity	99.3%;	Pred. No. 1.7e-213;		
Matches 425;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
QY	1	MATSGTGVFFMLVWSVCVSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMEDAGSGTGT	60	
DB	1	MATSGTGVFFMLVWSVCVSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMEDAGSGTGT	60	
QY	61	RIHYVTFVQKMPGQLPILLEGVFPDSVKPGLSAFVDQPKQGAETVGGLLEVAKDSIPRSHW	120	
DB	61	RIHYVTFVQKMPGQLPILLEGVFPDSVKPGLSAFVDQPKQGAETVGGLLEVAKDSIPRSHW	120	

121 KKTPTVVLKATAGRLRLPEHAKALLPEVKEIFRKSPLVPKGSVIMDGSDEGILLAWTV 180
 121 KKTPTVVLKATAGRLRLPEHAKALLPEVKEIFRKSPLVPKGSVIMDGSDEGILLAWTV 180
 181 NLTGQLHGRHROETVGTLDLGGASTQITFLPOFEKTLQTPRGYLTSEFNFNSTYKLYTH 240
 181 NLTGQLHGRHROETVGTLDLGGASTQITFLPOFEKTLQTPRGYLTSEFNFNSTYKLYTH 240
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 301 EPCYAEVLVRVGRKGLHQPVEVQSGFYAFSYDDRAVDTMDIDYKGGILKVEDFERKAR 360
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 361 EVCNLENFTSGSPFLCMLSYITALLKDGFGFADSTVLQ 420
 361 EVCNLENFTSGSPFLCMLSYITALLKDGFGFADSTVLQ 420
 421 LQSLGISH 428
 421 LQSLGISH 428

RESULT 12
 US-10-092-063-25
 ; Sequence 25, Application US/10092063
 ; Publication No. US20020173005A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ford, John
 ; APPLICANT: Mulero, Julio
 ; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
 ; FILE REFERENCE: 28110/35908
 ; CURRENT APPLICATION NUMBER: US/10/092.063
 ; CURRENT FILING DATE: 2002-03-05
 ; PRIOR APPLICATION NUMBER: 09/370,265
 ; PRIOR FILING DATE: 2002-01-31
 ; PRIOR APPLICATION NUMBER: PCT/US99/16180
 ; PRIOR FILING DATE: 1999-07-16
 ; PRIOR APPLICATION NUMBER: 09/350,836
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: 09/273,447
 ; PRIOR FILING DATE: 1999-03-19
 ; PRIOR APPLICATION NUMBER: 09/244,444
 ; PRIOR FILING DATE: 1999-02-04
 ; PRIOR APPLICATION NUMBER: 09/122,449
 ; PRIOR FILING DATE: 1998-07-24
 ; PRIOR APPLICATION NUMBER: 09/118,205
 ; PRIOR FILING DATE: 1998-07-16
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 25
 ; LENGTH: 405
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-092-063-25

Query Match 93.5%; Score 2104; DB 13; Length 405;
 Best Local Similarity 100.0%; Pred. No. 1.8e-200;
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 MATSWGTVPFVLMVSVCSAVSHRNQQTWFGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
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 61 RIHYTTFVQKMPGQLPILGEGVDFSVKPGLSAFVDPQKGAETVQGLLEVAKDSIPRSHW 120
 61 RIHYTTFVQKMPGQLPILGEGVDFSVKPGLSAFVDPQKGAETVQGLLEVAKDSIPRSHW 120
 121 KKTPTVVLKATAGRLRLPEHAKALLPEVKEIFRKSPLVPKGSVIMDGSDEGILLAWTV 180

121 KKTPTVVLKATAGRLRLPEHAKALLPEVKEIFRKSPLVPKGSVIMDGSDEGILLAWTV 180
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 241 SYLGFGKKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNOGEVGF 300
 301 EPCYAEVLVRVGRKGLHQPVEVQSGFYAFSYDDRAVDTMDIDYKGGILKVEDFERKAR 360
 301 EPCYAEVLVRVGRKGLHQPVEVQSGFYAFSYDDRAVDTMDIDYKGGILKVEDFERKAR 360
 361 EVCNLENFTSGSPFLCMLSYITALLKDGFGFADSTVLQ 400
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RESULT 13
 US-10-286-926-25
 ; Sequence 25, Application US/10286926
 ; Publication No. US20030175752A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ford, John
 ; APPLICANT: Mulero, Julio
 ; APPLICANT: Yeung, George
 ; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
 ; TITLE OF INVENTION: Polypeptides
 ; FILE REFERENCE: 28110/36457CON
 ; CURRENT APPLICATION NUMBER: US/10/286,926
 ; CURRENT FILING DATE: 2002-11-01
 ; PRIOR APPLICATION NUMBER: 09/557,800
 ; PRIOR FILING DATE: 2000-04-25
 ; PRIOR APPLICATION NUMBER: 09/481,238
 ; PRIOR FILING DATE: 2000-01-11
 ; PRIOR APPLICATION NUMBER: 09/370,265
 ; PRIOR FILING DATE: 1999-08-09
 ; PRIOR APPLICATION NUMBER: PCT/US99/16180
 ; PRIOR FILING DATE: 1999-07-16
 ; PRIOR APPLICATION NUMBER: 09/350,836
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: 09/273,447
 ; PRIOR FILING DATE: 1999-03-19
 ; PRIOR APPLICATION NUMBER: 09/122,449
 ; PRIOR FILING DATE: 1998-07-24
 ; PRIOR APPLICATION NUMBER: 09/244,444
 ; PRIOR FILING DATE: 1999-02-04
 ; PRIOR APPLICATION NUMBER: 09/118,205
 ; PRIOR FILING DATE: 1998-07-16
 ; NUMBER OF SEQ ID NOS: 54
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 25
 ; LENGTH: 405
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-286-926-25

Query Match 93.5%; Score 2104; DB 14; Length 405;
 Best Local Similarity 100.0%; Pred. No. 1.8e-200;
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 1 MATSWGTVPFVLMVSVCSAVSHRNQQTWFGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
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 61 RIHYTTFVQKMPGQLPILGEGVDFSVKPGLSAFVDPQKGAETVQGLLEVAKDSIPRSHW 120
 121 KKTPTVVLKATAGRLRLPEHAKALLPEVKEIFRKSPLVPKGSVIMDGSDEGILLAWTV 180
 121 KKTPTVVLKATAGRLRLPEHAKALLPEVKEIFRKSPLVPKGSVIMDGSDEGILLAWTV 180

QY 181 NFLTQGLHGRQETVGTDLGGASTQITFLPQFENKLEQTPRGYLTSEFNFSTYKLYTH 240
 DB 181 NFLTQGLHGRQETVGTDLGGASTQITFLPQFENKLEQTPRGYLTSEFNFSTYKLYTH 240
 QY 241 SYLGFGKAAARLATIAGLETGTGHTFRSACLPRLAEAWIFGGVKYQYGGNQGEGVGF 300
 DB 241 SYLGFGKAAARLATIAGLETGTGHTFRSACLPRLAEAWIFGGVKYQYGGNQGEGVGF 300
 QY 301 EPCVAEVLVRVGRKLGHPQEEVQRGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
 DB 301 EPCVAEVLVRVGRKLGHPQEEVQRGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
 QY 361 EVCNLENFTSGSPFLCNDLSYITALLKXGFGFADSTVLQ 400
 DB 361 EVCNLENFTSGSPFLCNDLSYITALLKXGFGFADSTVLQ 400

RESULT 14
 US-10-231-913-126
 ; Sequence 126, Application US/10231913
 ; Publication No. US20040005576A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Guo, Xiaojia S.
 ; APPLICANT: Li, Li
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Shinkets, Richard A.
 ; APPLICANT: Casman, Stacie J.
 ; APPLICANT: Malyankar, Uriel M.
 ; APPLICANT: Tchernev, Velizar T.
 ; APPLICANT: Vernet, Corine A.
 ; APPLICANT: Spytek, Kimberly A.
 ; APPLICANT: Shency, Suresh G.
 ; APPLICANT: Alsobrook II, John P.
 ; APPLICANT: Edinger, Schlomit
 ; APPLICANT: Feyman, John A.
 ; APPLICANT: Stone, David J.
 ; APPLICANT: Ellerman, Karen
 ; APPLICANT: Gangolli, Esha A.
 ; APPLICANT: Boldog, Ference L.
 ; APPLICANT: Colman, Steven D.
 ; APPLICANT: Eisen, Andrew J.
 ; APPLICANT: Liu, Xiaohong
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Spaderna, Steven K.
 ; APPLICANT: Zerhusen, Bryan D.
 ; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 21402-216
 ; CURRENT APPLICATION NUMBER: US/10/231,913
 ; CURRENT FILING DATE: 2002-08-30
 ; PRIOR APPLICATION NUMBER: 60/251,660
 ; PRIOR FILING DATE: 2000-12-06
 ; PRIOR APPLICATION NUMBER: 60/255,029
 ; PRIOR FILING DATE: 2000-12-12
 ; PRIOR APPLICATION NUMBER: 60/260,326
 ; PRIOR FILING DATE: 2001-01-08
 ; PRIOR APPLICATION NUMBER: 60/263,800
 ; PRIOR FILING DATE: 2001-01-24
 ; PRIOR APPLICATION NUMBER: 60/269,942
 ; PRIOR FILING DATE: 2001-02-20
 ; PRIOR APPLICATION NUMBER: 60/286,183
 ; PRIOR FILING DATE: 2001-04-24
 ; PRIOR APPLICATION NUMBER: 60/313,627
 ; PRIOR FILING DATE: 2001-08-20
 ; PRIOR APPLICATION NUMBER: 60/318,712
 ; PRIOR FILING DATE: 2001-09-12
 ; NUMBER OF SEQ ID NOS: 292
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 126
 ; TYPE: PRT
 ; LENGTH: 427
 ; ORGANISM: Mus musculus
 US-10-231-913-126

Query Match 88.6%; Score 1994.5; DB 15; Length 427;
 Best Local Similarity 88.3%; Pred. No. 1.6e-189;
 Matches 377; Conservative 24; Mismatches 25; Indels 1; Gaps 1;
 QY 1 MATSWGVVPMVLVVCVCSAVSHRNQOTWPEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
 DB 1 MATSWGNV-PALLIACVGSIVFYREQQWPEGVFLSSMCPINVSAGTFYGINFDAGSTGT 59
 QY 61 RIHYTVPQKQGPQLPILEGEVFTDSVKPGLSFAVDQPKQGAETVQGLLEVAKDSIPRSHW 120
 DB 60 RIHYTVPQKQGPQLPILEGEVFTDSVKPGLSFAVDQPKQGAETVQGLLEVAKDSIPRSHW 119
 QY 121 KKTVPVLKATAGRLLEPEHAKALLPEVKEIFPKSPFLVPKGSVIMDGSDEGILAWTV 180
 DB 120 ERTPVVLKATAGRLLEPEHAKALLPEVKEIFPKSPFLVPKGSVIMDGSDEGILAWTV 179
 QY 181 NFLTQGLHGRQETVGTDLGGASTQITFLPQFENKLEQTPRGYLTSEFNFSTYKLYTH 240
 DB 180 NFLTQGLHGRQETVGTDLGGASTQITFLPQFENKLEQTPRGYLTSEFNFSTYKLYTH 239
 QY 241 SYLGFGKAAARLATIAGLETGTGHTFRSACLPRLAEAWIFGGVKYQYGGNQGEGVGF 300
 DB 240 SYLGFGKAAARLATIAGLETGTGHTFRSACLPRLAEAWIFGGVKYQYGGNQGEGVGF 299
 QY 301 EPCVAEVLVRVGRKLGHPQEEVQRGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
 DB 300 EPCVAEVLVRVGRKLGHPQEEVQRGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 359
 QY 361 EVCNLENFTSGSPFLCNDLSYITALLKXGFGFADSTVLQITKKVNNIETGWALGATFHL 420
 DB 360 EVCNLENFTSGSPFLCNDLSYITALLKXGFGFADSTVLQITKKVNNIETGWALGATFHL 419
 QY 421 LQSLGIS 427
 DB 420 LQSLGIT 426
 RESULT 15
 US-10-092-063-39
 ; Sequence 39, Application US/10092063
 ; Publication No. US20020173005A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ford, John
 ; APPLICANT: Mulero, Julio
 ; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDE
 ; FILE REFERENCE: 28116/35908
 ; CURRENT APPLICATION NUMBER: US/10/092,063
 ; CURRENT FILING DATE: 2002-03-05
 ; PRIOR APPLICATION NUMBER: 09/370,265
 ; PRIOR FILING DATE: 2002-01-31
 ; PRIOR APPLICATION NUMBER: PCT/US99/16180
 ; PRIOR FILING DATE: 1999-07-16
 ; PRIOR APPLICATION NUMBER: 09/350,836
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: 09/273,447
 ; PRIOR FILING DATE: 1999-03-19
 ; PRIOR APPLICATION NUMBER: 09/244,444
 ; PRIOR FILING DATE: 1999-02-04
 ; PRIOR APPLICATION NUMBER: 09/122,449
 ; PRIOR FILING DATE: 1998-07-24
 ; PRIOR APPLICATION NUMBER: 09/118,205
 ; PRIOR FILING DATE: 1998-07-16
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 39
 ; TYPE: PRT
 ; LENGTH: 465
 ; ORGANISM: Mus musculus
 US-10-092-063-39
 Query Match 81.7%; Score 1837.5; DB 13; Length 465;
 Best Local Similarity 84.0%; Pred. No. 7.8e-174;

Thu Jul 1 14:44:04 2004

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Db	1	MATSWGAV-FML::ACVGSVTFVREQQTWFEGVFFSSMCPINVSAGTGYGIIMFDAGSTGT	59						
Qy	61	RIHYTTFVQKMPGOLPILEGEVPSVKPGLSAFVQPKQGAETVQGLLEVAKDISIPRSHW	120						
Db	60	RIHYTTFVQKTAGOLPILEGEIPDSVKPGLSAFVQPKQGAETVQGLLEVAKDISIPRSHW	119						
Qy	121	KKTIPWLKATAGRLIPEHKAKALLPEVXEIPFKSPFLVPKGSVSIIMDGSDEGILAWTV	180						
Db	120	ERTPWLKATAGRLIPEKSAQALLVEBEIPKNSPFLVPDGSVSIIMDGSYEGILAWTV	179						
Qy	181	NFLTQGLHGRQETVGTLDLGGASTQITFLPQPEKTELETPRGYILTSPEMFSNTYKLYTH	240						
Db	180	NFLTQGLHGRQETVGTLDLGGASTQITFLPQPEKTELETPRGYILTSPEMFSNTYKLYTH	239						
Qy	241	SYLGFGKKAARLATLGALETGTGDTGHTFFRSACLPRMLEAEMFGGVKTYQYGNQGEVGF	300						
Db	240	SYLGFGKKAARLATLGALEAKGTGHTFFRSACLPRMLEAEMFGGVKTYQYGNQGEVGF	299						
Qy	301	EPCYAEVLVRVGRKLGHPERVQRGSFYATSYYYDVRAVDTMDIYKGGILKVVDEPERKAR	360						
Db	300	EPCYAEVLVRVQGRKLHQPEEVVRGSFYATSYYYDRAADTHLIDYKGGYKLVKVEDPERKAR	359						
Qy	361	EVCNDLENFTSGSFFLCMDLSYITLNLKDGFGFADSTVLQTLTKVNNITFGWALCATPHL	420						
Db	360	EVCNDENGSFSSGSFFLCMDLYITALLKQGLGAERHPITTAHKV-SEQUEDW-LGLGGLH	417						

Search completed: July 1, 2004, 13:58:40
Job time : 46.5 secs

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OM protein - protein search, using sw model

Run on: July 1, 2004, 13:44:42 ; Search time 16.5 Seconds
(without alignments)
1339.146 Million cell updates/sec

Title: US-10-091-085-7

Perfect score: 2252

Sequence: 1 MATSGTGVFFMLVSVCSA.....ETGWLGAFTFLQLSLGISH 428

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
- 1: /cgm2_6/ptodata/2/iaa/5A.COMB.pep.*
 - 2: /cgm2_6/ptodata/2/iaa/5B.COMB.pep.*
 - 3: /cgm2_6/ptodata/2/iaa/6A.COMB.pep.*
 - 4: /cgm2_6/ptodata/2/iaa/6B.COMB.pep.*
 - 5: /cgm2_6/ptodata/2/iaa/PTUS.COMB.pep.*
 - 6: /cgm2_6/ptodata/2/iaa/backfilest.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2252	100.0	428	4	US-09-608-285A-7
2	2252	100.0	428	4	US-09-350-836B-7
3	2252	100.0	428	4	US-09-370-265-7
4	2252	100.0	428	4	US-09-557-800C-7
5	2252	100.0	428	4	US-09-370-625A-7
6	2235	99.2	428	4	US-09-608-285A-3
7	2235	99.2	428	4	US-09-608-285A-5
8	2235	99.2	428	4	US-09-240-639-6
9	2235	99.2	428	4	US-09-240-639-9
10	2235	99.2	428	4	US-09-350-836B-3
11	2235	99.2	428	4	US-09-350-836B-5
12	2235	99.2	428	4	US-09-370-265-3
13	2235	99.2	428	4	US-09-370-265-5
14	2235	99.2	428	4	US-09-557-800C-3
15	2235	99.2	428	4	US-09-557-800C-5
16	2235	99.2	428	4	US-09-370-625A-3
17	2235	99.2	428	4	US-09-370-625A-5
18	2089	92.8	405	4	US-09-608-285A-25
19	2089	92.8	405	4	US-09-370-265-25
20	2089	92.8	405	4	US-09-557-800C-25
21	2089	92.8	405	4	US-09-370-625A-25
22	1822.5	80.9	465	4	US-09-557-800C-56
23	1822.5	80.9	465	4	US-09-370-625A-39
24	1817.5	80.7	465	4	US-09-240-639-8
25	996	44.2	456	4	US-09-240-639-2
26	996	44.2	484	4	US-09-608-285A-27
27	996	44.2	484	4	US-09-370-265-27

28	996	44.2	484	4	US-09-557-800C-27	Sequence 27, Appl
29	996	44.2	484	4	US-09-370-625A-27	Sequence 27, Appl
30	816.5	36.3	471	4	US-09-608-285A-50	Sequence 60, Appl
31	507.5	22.3	467	4	US-09-129-112-19	Sequence 19, Appl
32	502.5	22.3	459	4	US-09-129-112-9	Sequence 9, Appl
33	493	21.9	462	4	US-09-129-112-2	Sequence 2, Appl
34	486.5	21.6	462	4	US-09-129-112-15	Sequence 15, Appl
35	484	21.5	455	4	US-09-240-639-10	Sequence 10, Appl
36	472.5	21.0	473	4	US-09-240-639-12	Sequence 12, Appl
37	441.5	19.6	454	4	US-09-240-639-11	Sequence 11, Appl
38	366	16.3	502	4	US-09-557-800C-55	Sequence 55, Appl
39	366	16.3	502	4	US-09-370-625A-38	Sequence 38, Appl
40	366	16.3	510	3	US-08-930-921-1	Sequence 1, Appl
41	357.5	15.9	529	4	US-09-240-639-4	Sequence 4, Appl
42	229	10.2	148	4	US-09-240-639-17	Sequence 17, Appl
43	201	8.9	153	4	US-09-240-639-13	Sequence 13, Appl
44	191	8.5	153	4	US-09-240-639-15	Sequence 15, Appl
45	189.5	8.4	150	4	US-09-240-639-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-608-285A-7
; Sequence 7, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: ~~Fora~~, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-608-285A-7

Query Match 100.0% Score 2252; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 7,8e-247; Indels 0; Gaps 0;
Matches 428; Conservative 0; Mismatches 0;
QY 1 MATSGTGVFFMLVSVCSA VSHRNQQTWTFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
Db 1 MATSGTGVFFMLVSVCSA VSHRNQQTWTFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
QY 61 RIHVYTFVQKMPGQLPILEGEVDSVKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120

Db 181 NLTGQLHGRQETVGTLDLGGASTQITFLPQFETLQTPRGYLTSEMFNSTYKLYTH 240
Qy 241 SYLGFGGLKAARLALATLGALETGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
Db 241 SYLGFGGLKAARLALATLGALETGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
Qy 301 EPCYAEVLVRVGRKQHQPVEVQSGSFYAFSYDDRAVDTDMDYKGGILKVEDFERKAR 360
Db 301 EPCYAEVLVRVGRKQHQPVEVQSGSFYAFSYDDRAVDTDMDYKGGILKVEDFERKAR 360
Qy 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQTKKNNIETGVALGATFHL 420
Db 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQTKKNNIETGVALGATFHL 420
Qy 421 LOSLGISH 428
Db 421 LOSLGISH 428

RESULT 3
US-09-370-265-7
; Sequence 7, Application US/09370265
; Patent No. 6447771
; GENERAL INFORMATION:
; APPLICANT: Mulero, John
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; FILE REFERENCE: 28111/35908
; CURRENT APPLICATION NUMBER: US/09/370,265
; EARLIER FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: PCT/US99/16180
; EARLIER FILING DATE: 1999-07-16
; EARLIER APPLICATION NUMBER: 09/350,836
; EARLIER FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: 09/273,447
; EARLIER FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: 09/244,444
; EARLIER FILING DATE: 1999-02-04
; EARLIER APPLICATION NUMBER: 09/122,449
; EARLIER FILING DATE: 1998-07-24
; EARLIER APPLICATION NUMBER: 09/118,205
; EARLIER FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-370-265-7

Query Match 100.0%; Score 2252; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 7.8e-247;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATSWGTVPFVFLVWVCVCSAVSHRNOQTWFEGLFLSSMCPINVSASTLYGINFDAGSTGT 60
Db 1 MATSWGTVPFVFLVWVCVCSAVSHRNOQTWFEGLFLSSMCPINVSASTLYGINFDAGSTGT 60
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Db 61 RIHVYTFVQKMPGQLPILEGEVFDVSKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
Qy 121 KKTPTVVKATAGLRLPEHAKALLFEVKEIFRKSPLVPKGSVIMTGDEGIFAWVTV 180
Db 121 KKTPTVVKATAGLRLPEHAKALLFEVKEIFRKSPLVPKGSVIMTGDEGIFAWVTV 180
Qy 181 NLTGQLHGRQETVGTLDLGGASTQITFLPQFETLQTPRGYLTSEMFNSTYKLYTH 240
Db 181 NLTGQLHGRQETVGTLDLGGASTQITFLPQFETLQTPRGYLTSEMFNSTYKLYTH 240
Qy 241 SYLGFGGLKAARLALATLGALETGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300

Db 61 RIHVYTFVQKMPGQLPILEGEVFDVSKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
Qy 121 KKTPTVVKATAGLRLPEHAKALLFEVKEIFRKSPLVPKGSVIMTGDEGIFAWVTV 180
Db 121 KKTPTVVKATAGLRLPEHAKALLFEVKEIFRKSPLVPKGSVIMTGDEGIFAWVTV 180
Qy 181 NLTGQLHGRQETVGTLDLGGASTQITFLPQFETLQTPRGYLTSEMFNSTYKLYTH 240
Db 181 NLTGQLHGRQETVGTLDLGGASTQITFLPQFETLQTPRGYLTSEMFNSTYKLYTH 240
Qy 241 SYLGFGGLKAARLALATLGALETGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
Db 241 SYLGFGGLKAARLALATLGALETGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
Qy 301 EPCYAEVLVRVGRKQHQPVEVQSGSFYAFSYDDRAVDTDMDYKGGILKVEDFERKAR 360
Db 301 EPCYAEVLVRVGRKQHQPVEVQSGSFYAFSYDDRAVDTDMDYKGGILKVEDFERKAR 360
Qy 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQTKKNNIETGVALGATFHL 420
Db 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQTKKNNIETGVALGATFHL 420
Qy 421 LOSLGISH 428
Db 421 LOSLGISH 428

RESULT 2
US-09-350-836B-7
; Sequence 7, Application US/09350836B
; Patent No. 638745
; GENERAL INFORMATION:
; APPLICANT: Mulero, John
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; FILE REFERENCE: 28110/35761
; CURRENT APPLICATION NUMBER: US/09/350,836B
; CURRENT FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-350-836B-7

Query Match 100.0%; Score 2252; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 7.8e-247;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MATSWGTVPFVFLVWVCVCSAVSHRNOQTWFEGLFLSSMCPINVSASTLYGINFDAGSTGT 60
Db 1 MATSWGTVPFVFLVWVCVCSAVSHRNOQTWFEGLFLSSMCPINVSASTLYGINFDAGSTGT 60
Qy 61 RIHVYTFVQKMPGQLPILEGEVFDVSKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
Db 61 RIHVYTFVQKMPGQLPILEGEVFDVSKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
Qy 121 KKTPTVVKATAGLRLPEHAKALLFEVKEIFRKSPLVPKGSVIMTGDEGIFAWVTV 180
Db 121 KKTPTVVKATAGLRLPEHAKALLFEVKEIFRKSPLVPKGSVIMTGDEGIFAWVTV 180
Qy 181 NLTGQLHGRQETVGTLDLGGASTQITFLPQFETLQTPRGYLTSEMFNSTYKLYTH 240

Db 301 BPCYAEVLVRGKLHQPEEVQSGFYAFSVYVYDRAVDTMDIDYKGGILKVEDFERKAR 360
QY 361 EVCNLENFTSGSPFLCMDLSYITALLKDGEGFADSTVLQLTKKVNNIETGHALGATPHL 420
Db 361 EVCNLENFTSGSPFLCMDLSYITALLKDGEGFADSTVLQLTKKVNNIETGHALGATPHL 420
QY 421 LQSLGISH 428
Db 421 LQSLGISH 428

RESULT 7

US-09-608-285A-5
; Sequence 5, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-608-285A-5

Query Match 99.2%; Score 2235; DB 4; Length 428;
Best Local Similarity 99.3%; Pred. No. 6.7e-245; Indels 0; Gaps 0;
Matches 425; Conservative 0; Mismatches 3;

QY 1 MATSNGTVFFMLVWSCVSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
Db 1 MATSNGTVFFMLVWSCVSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
QY 61 RIHYTVFVQKMGQPLILEGEVFDSPKGLSAFVDPQKGAETVQGLLEVAKDSIPRSHW 120
Db 61 RIHYTVFVQKMGQPLILEGEVFDSPKGLSAFVDPQKGAETVQGLLEVAKDSIPRSHW 120
QY 121 KKTVPVLKATAGLRLLPEHKAALIFEVKEIFRKSPFLVPKGSVSIMTQDEGIPAWTV 180
Db 121 KKTVPVLKATAGLRLLPEHKAALIFEVKEIFRKSPFLVPKGSVSIMTQDEGIPAWTV 180
QY 181 NFLTQGLHGRQETVGTLDLGGASTQITFLPQFKTEOTPRGYLTSPFEMNSTYKLYTH 240
Db 181 NFLTQGLHGRQETVGTLDLGGASTQITFLPQFKTEOTPRGYLTSPFEMNSTYKLYTH 240
QY 241 SYLGFGLKAARLTIAGLETGTDGHTFRSACLPRWLEAEWIFGVKTYQGNQGEVGF 300

QY 421 LQSLGISH 428
Db 421 LQSLGISH 428

RESULT 6

US-09-608-285A-3
; Sequence 3, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-608-285A-3

Query Match 99.2%; Score 2235; DB 4; Length 428;
Best Local Similarity 99.3%; Pred. No. 6.7e-245; Indels 0; Gaps 0;
Matches 425; Conservative 0; Mismatches 3;

QY 1 MATSNGTVFFMLVWSCVSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
Db 1 MATSNGTVFFMLVWSCVSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
QY 61 RIHYTVFVQKMGQPLILEGEVFDSPKGLSAFVDPQKGAETVQGLLEVAKDSIPRSHW 120
Db 61 RIHYTVFVQKMGQPLILEGEVFDSPKGLSAFVDPQKGAETVQGLLEVAKDSIPRSHW 120
QY 121 KKTVPVLKATAGLRLLPEHKAALIFEVKEIFRKSPFLVPKGSVSIMTQDEGIPAWTV 180
Db 121 KKTVPVLKATAGLRLLPEHKAALIFEVKEIFRKSPFLVPKGSVSIMTQDEGIPAWTV 180
QY 181 NFLTQGLHGRQETVGTLDLGGASTQITFLPQFKTEOTPRGYLTSPFEMNSTYKLYTH 240
Db 181 NFLTQGLHGRQETVGTLDLGGASTQITFLPQFKTEOTPRGYLTSPFEMNSTYKLYTH 240
QY 241 SYLGFGLKAARLTIAGLETGTDGHTFRSACLPRWLEAEWIFGVKTYQGNQGEVGF 300
Db 241 SYLGFGLKAARLTIAGLETGTDGHTFRSACLPRWLEAEWIFGVKTYQGNQGEVGF 300
QY 301 BPCYAEVLVRGKLHQPEEVQSGFYAFSVYVYDRAVDTMDIDYKGGILKVEDFERKAR 360

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Db      241 SYLGFGLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
QY      301 EPCYAEVLVRVGRKQHQPVEEVQSGFYAFSYFYDRAVDTMDIDYKGGILKVEDFERKAR 360
Db      301 EPCYAEVLVRVGRKQHQPVEEVQSGFYAFSYFYDRAVDTMDIDYKGGILKVEDFERKAR 360
QY      361 EVCMDLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQTKKNNIETGWLGAATFHL 420
Db      361 EVCMDLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQTKKNNIETGWLGAATFHL 420
QY      421 LOSLGISH 428
Db      421 LOSLGISH 428

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RESULT 8
US-09-240-639-5
; Sequence 6, Application US/09240639
; Patent No. 6350447
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischaut, Anna-Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/240,639
; CURRENT FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-240-639-5

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Query Match      99.2%; Score 2235; DB 4; Length 428;
Best Local Similarity 99.3%; Sred. No. 6.7e-245;
Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 MATSNGTTFVFMVWSCVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
Db      1 MATSNGTTFVFMVWSCVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
QY      61 RIHVYTFVQKMPGQQLPILGEVFDVSKPGLSAFVDQPKQGAETVQGLLEVAKOSIPRSHW 120
Db      61 RIHVYTFVQKMPGQQLPILGEVFDVSKPGLSAFVDQPKQGAETVQGLLEVAKOSIPRSHW 120
QY      121 KKTPTVLKATAGLRLLPEHKAKALLFEVKEIFRKSPPFLVPKGSVSIIMTGDGEPANVTY 180
Db      121 KKTPTVLKATAGLRLLPEHKAKALLFEVKEIFRKSPPFLVPKGSVSIIMTGDGEPANVTY 180
QY      181 NFLTQQLHGRQETVGTGLDGGASTQITFLPQPKXTLEQTPRGYLTSPFEMFNSTYKLYTH 240
Db      181 NFLTQQLHGRQETVGTGLDGGASTQITFLPQPKXTLEQTPRGYLTSPFEMFNSTYKLYTH 240
QY      241 SYLGFGLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
Db      241 SYLGFGLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
QY      301 EPCYAEVLVRVGRKQHQPVEEVQSGFYAFSYFYDRAVDTMDIDYKGGILKVEDFERKAR 360
Db      301 EPCYAEVLVRVGRKQHQPVEEVQSGFYAFSYFYDRAVDTMDIDYKGGILKVEDFERKAR 360
QY      361 EVCMDLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQTKKNNIETGWLGAATFHL 420
Db      361 EVCMDLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQTKKNNIETGWLGAATFHL 420
QY      421 LOSLGISH 428
Db      421 LOSLGISH 428

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RESULT 9
US-09-240-639-9
; Sequence 9, Application US/09240639
; Patent No. 6350447
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischaut, Anna-Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/240,639
; CURRENT FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 9
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-240-639-9

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Query Match      99.2%; Score 2235; DB 4; Length 428;
Best Local Similarity 99.3%; Pred. No. 6.7e-245;
Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 MATSNGTTFVFMVWSCVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
Db      1 MATSNGTTFVFMVWSCVCSAVSHRNQQTWFEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
QY      61 RIHVYTFVQKMPGQQLPILGEVFDVSKPGLSAFVDQPKQGAETVQGLLEVAKOSIPRSHW 120
Db      61 RIHVYTFVQKMPGQQLPILGEVFDVSKPGLSAFVDQPKQGAETVQGLLEVAKOSIPRSHW 120
QY      121 KKTPTVLKATAGLRLLPEHKAKALLFEVKEIFRKSPPFLVPKGSVSIIMTGDGEPANVTY 180
Db      121 KKTPTVLKATAGLRLLPEHKAKALLFEVKEIFRKSPPFLVPKGSVSIIMTGDGEPANVTY 180
QY      181 NFLTQQLHGRQETVGTGLDGGASTQITFLPQPKXTLEQTPRGYLTSPFEMFNSTYKLYTH 240
Db      181 NFLTQQLHGRQETVGTGLDGGASTQITFLPQPKXTLEQTPRGYLTSPFEMFNSTYKLYTH 240
QY      241 SYLGFGLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
Db      241 SYLGFGLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEGF 300
QY      301 EPCYAEVLVRVGRKQHQPVEEVQSGFYAFSYFYDRAVDTMDIDYKGGILKVEDFERKAR 360
Db      301 EPCYAEVLVRVGRKQHQPVEEVQSGFYAFSYFYDRAVDTMDIDYKGGILKVEDFERKAR 360
QY      361 EVCMDLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQTKKNNIETGWLGAATFHL 420
Db      361 EVCMDLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQTKKNNIETGWLGAATFHL 420
QY      421 LOSLGISH 428
Db      421 LOSLGISH 428

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RESULT 10
US-09-350-836B-3
; Sequence 3, Application US/09350836B
; Patent No. 6387645
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/35761
; CURRENT APPLICATION NUMBER: US/09/350,836B
; CURRENT FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16

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; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-350-836B-3

Query Match 99.2%; Score 2235; DB 4; Length 428;
Best Local Similarity 99.3%; Pred. No. 6.7e-245;
Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MATSWGTVPFVLMVSVCSAVSHRNQQTWFEIGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSWGTVPFVLMVSVCSAVSHRNQQTWFEIGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
QY 61 RIHYVTFVQKMPGQLPILGEVFDVSVKPGLSAFVDPQKQGAETVQGLLEVAKDSIPRSHW 120
DB 61 RIHYVTFVQKMPGQLPILGEVFDVSVKPGLSAFVDPQKQGAETVQGLLEVAKDSIPRSHW 120
QY 121 KKTTPVVKATAGLRLPEHKAKALLPEVKEIFRKSPLVPKGSVSIIMDGSDEGILAWTV 180
DB 121 KKTTPVVKATAGLRLPEHKAKALLPEVKEIFRKSPLVPKGSVSIIMDGSDEGILAWTV 180
QY 181 NFLTQGLHGRQETVGTLDLGASTQITFLPQFEKTLQTPRGYLTSPFEMNSTYKLYTH 240
DB 181 NFLTQGLHGRQETVGTLDLGASTQITFLPQFEKTLQTPRGYLTSPFEMNSTYKLYTH 240
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DB 241 SYLPGGLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEVF 300
QY 301 EPCYAEVLVRVVRGKLHQPBEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
DB 301 EPCYAEVLVRVVRGKLHQPBEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
QY 361 EVCNDLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQTKKVNNIETGWLGAFTFHL 420
DB 361 EVCNDLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQTKKVNNIETGWLGAFTFHL 420
QY 421 LQSLGISH 428
DB 421 LQSLGISH 428

RESULT 11
US-09-350-836B-5
; Sequence 5, Application US/09350836B
; Patent No. 6387645
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; FILE REFERENCE: 28110/35761
; CURRENT APPLICATION NUMBER: US/09/350,836B
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 428

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-350-836B-5

Query Match 99.2%; Score 2235; DB 4; Length 428;
Best Local Similarity 99.3%; Pred. No. 6.7e-245;
Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MATSWGTVPFVLMVSVCSAVSHRNQQTWFEIGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSWGTVPFVLMVSVCSAVSHRNQQTWFEIGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
QY 61 RIHYVTFVQKMPGQLPILGEVFDVSVKPGLSAFVDPQKQGAETVQGLLEVAKDSIPRSHW 120
DB 61 RIHYVTFVQKMPGQLPILGEVFDVSVKPGLSAFVDPQKQGAETVQGLLEVAKDSIPRSHW 120
QY 121 KKTTPVVKATAGLRLPEHKAKALLPEVKEIFRKSPLVPKGSVSIIMDGSDEGILAWTV 180
DB 121 KKTTPVVKATAGLRLPEHKAKALLPEVKEIFRKSPLVPKGSVSIIMDGSDEGILAWTV 180
QY 181 NFLTQGLHGRQETVGTLDLGASTQITFLPQFEKTLQTPRGYLTSPFEMNSTYKLYTH 240
DB 181 NFLTQGLHGRQETVGTLDLGASTQITFLPQFEKTLQTPRGYLTSPFEMNSTYKLYTH 240
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DB 241 SYLPGGLKAARLATLGALETGTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEVF 300
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DB 301 EPCYAEVLVRVVRGKLHQPBEVQSGSFYAFSYYYDRAVDTMDIDYKGGILKVEDFERKAR 360
QY 361 EVCNDLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQTKKVNNIETGWLGAFTFHL 420
DB 361 EVCNDLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQTKKVNNIETGWLGAFTFHL 420
QY 421 LQSLGISH 428
DB 421 LQSLGISH 428

RESULT 12
US-09-370-265-3
; Sequence 3, Application US/09370265
; Patent No. 6447771
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; FILE REFERENCE: 28111/35908
; CURRENT APPLICATION NUMBER: US/09/370,265
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: PCT/US99/16180
; EARLIER FILING DATE: 1999-07-16
; EARLIER APPLICATION NUMBER: 09/350,836
; EARLIER FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: 09/273,447
; EARLIER FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: 09/244,444
; EARLIER FILING DATE: 1999-02-04
; EARLIER APPLICATION NUMBER: 09/122,449
; EARLIER FILING DATE: 1998-07-24
; EARLIER APPLICATION NUMBER: 09/118,205
; EARLIER FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-370-265-3

Query Match 99.2%; Score 2235; DB 4; Length 428;
Best Local Similarity 99.3%; Pred. No. 6.7e-245; Indels 0; Gaps 0;
Matches 425; Conservative 0; Mismatches 3;

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DB 1 MATSWGTVPFVFWLWVSCVSAVSHRNQQTWFGIFLSSMCPINVSASTLYGIMFDAGSTGT 60

QY 61 RIHVYTFVQKMPGOLPILLEGVFDVSKPGLSAFVDPQKGAETVQGLLEVAKXDSIPRSHW 120
DB 61 RIHVYTFVQKMPGOLPILLEGVFDVSKPGLSAFVDPQKGAETVQGLLEVAKXDSIPRSHW 120

QY 121 KKTVPVVLKATAGRLRLPEHKAKALLFEVKEIPRKSFPFLVPKGSVIMTGDGEGIFAWTV 180
DB 121 KKTVPVVLKATAGRLRLPEHKAKALLFEVKEIPRKSFPFLVPKGSVIMTGDGEGIFAWTV 180

QY 181 NFLTQGLHGHROBTGTGTLGGASTQITFLPOFEKTLQTPRGVLTSPFENSTYKLYTH 240
DB 181 NFLTQGLHGHROBTGTGTLGGASTQITFLPOFEKTLQTPRGVLTSPFENSTYKLYTH 240

QY 241 SYLGFGLKAARLATLGALETGTDGHTFRSACLPRMLEAEWIFGGVKYQYGGNQEVEVF 300
DB 241 SYLGFGLKAARLATLGALETGTDGHTFRSACLPRMLEAEWIFGGVKYQYGGNQEVEVF 300

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DB 301 EPCYAEVLVRVGRKGLHQPVEVQSGFYAFSYYYDRAVDTMDIYKGGILKVEDFERKAR 360

QY 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQTKKVNNIETGVALGATFHL 420
DB 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQTKKVNNIETGVALGATFHL 420

QY 421 LQSLGISH 428
DB 421 LQSLGISH 428

RESULT 13
US-09-370-265-5
; Sequence 5, Application US/09370265
; Patent No. 6447771
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; FILE REFERENCE: 28111/35908
; CURRENT APPLICATION NUMBER: US/09/370,265
; EARLIER FILING DATE: 1999-08-09
; EARLIER FILING DATE: 1999-07-16
; EARLIER FILING DATE: 1999-07-09
; EARLIER FILING DATE: 1999-03-19
; EARLIER FILING DATE: 1999-02-04
; EARLIER FILING DATE: 1998-07-24
; EARLIER FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-370-265-5

Query Match 99.2%; Score 2235; DB 4; Length 428;
Best Local Similarity 99.3%; Pred. No. 6.7e-245; Indels 0; Gaps 0;
Matches 425; Conservative 0; Mismatches 3;

QY 1 MATSWGTVPFVFWLWVSCVSAVSHRNQQTWFGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSWGTVPFVFWLWVSCVSAVSHRNQQTWFGIFLSSMCPINVSASTLYGIMFDAGSTGT 60

QY 61 RIHVYTFVQKMPGOLPILLEGVFDVSKPGLSAFVDPQKGAETVQGLLEVAKXDSIPRSHW 120
DB 61 RIHVYTFVQKMPGOLPILLEGVFDVSKPGLSAFVDPQKGAETVQGLLEVAKXDSIPRSHW 120

QY 121 KKTVPVVLKATAGRLRLPEHKAKALLFEVKEIPRKSFPFLVPKGSVIMTGDGEGIFAWTV 180
DB 121 KKTVPVVLKATAGRLRLPEHKAKALLFEVKEIPRKSFPFLVPKGSVIMTGDGEGIFAWTV 180

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DB 181 NFLTQGLHGHROBTGTGTLGGASTQITFLPOFEKTLQTPRGVLTSPFENSTYKLYTH 240

QY 241 SYLGFGLKAARLATLGALETGTDGHTFRSACLPRMLEAEWIFGGVKYQYGGNQEVEVF 300
DB 241 SYLGFGLKAARLATLGALETGTDGHTFRSACLPRMLEAEWIFGGVKYQYGGNQEVEVF 300

QY 301 EPCYAEVLVRVGRKGLHQPVEVQSGFYAFSYYYDRAVDTMDIYKGGILKVEDFERKAR 360
DB 301 EPCYAEVLVRVGRKGLHQPVEVQSGFYAFSYYYDRAVDTMDIYKGGILKVEDFERKAR 360

QY 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQTKKVNNIETGVALGATFHL 420
DB 361 EVCNLENFTSGSPFLCNDLSYITALLKDGFGFADSTVLQTKKVNNIETGVALGATFHL 420

QY 421 LQSLGISH 428
DB 421 LQSLGISH 428

RESULT 14
US-09-557-800C-3
; Sequence 3, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR FILING DATE: 2000-01-11
; PRIOR FILING DATE: 1999-08-09
; PRIOR FILING DATE: 1999-07-16
; PRIOR FILING DATE: 1999-07-09
; PRIOR FILING DATE: 1999-03-19
; PRIOR FILING DATE: 1998-07-24
; PRIOR FILING DATE: 1998-07-16
; PRIOR FILING DATE: 1998-07-09
; PRIOR FILING DATE: 1998-07-16
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-557-800C-3

Query Match 99.2%; Score 2235; DB 4; Length 428;
Best Local Similarity 99.3%; Pred. No. 6.7e-245; Indels 0; Gaps 0;
Matches 425; Conservative 0; Mismatches 3;

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DB 61 RIHVYTFVQKMPGQOLPILEGVFDVSKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
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DB 121 KKTPTVWLKATAGLRLLPEHKAALLFEVKEIFRKSPPFLVPKGSVSIMTQDEGIFAWVTV 180
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DB 181 NFLTQGLHGRQETVGTLDLGGASTQITFLPQFEKTLROTGRYLTSFEMFNSTYKLYTH 240
QY 241 SYLGFGGLKAARLATIAGLETGDTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEVGF 300
DB 241 SYLGFGGLKAARLATIAGLETGDTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEVGF 300
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DB 361 EVCNDLENFTSGSPFLCNDLSYITALLXDGFGFADSTVLQLTKKVNNIETGALGATFHL 420
QY 421 LQSLGISH 428
DB 421 LQSLGISH 428
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RESULT 15
US-09-557-800C-5
; Sequence S, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Mulero, John
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-557-800C-5
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Query Match 99.2%; Score 2235; DB 4; Length 428;
Best Local Similarity 99.3%; Pred. No. 6,7e-245;

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Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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DB 61 RIHVYTFVQKMPGQOLPILEGVFDVSKPGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHW 120
QY 121 KKTPTVWLKATAGLRLLPEHKAALLFEVKEIFRKSPPFLVPKGSVSIMTQDEGIFAWVTV 180
DB 121 KKTPTVWLKATAGLRLLPEHKAALLFEVKEIFRKSPPFLVPKGSVSIMTQDEGIFAWVTV 180
QY 181 NFLTQGLHGRQETVGTLDLGGASTQITFLPQFEKTLROTGRYLTSFEMFNSTYKLYTH 240
DB 181 NFLTQGLHGRQETVGTLDLGGASTQITFLPQFEKTLROTGRYLTSFEMFNSTYKLYTH 240
QY 241 SYLGFGGLKAARLATIAGLETGDTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEVGF 300
DB 241 SYLGFGGLKAARLATIAGLETGDTGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEVEVGF 300
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DB 301 EPCYAEVLVVRGKLGHPBEVQSGSFYAFSYYDRAVDTMDIDYKGGILKVEDFERKAR 360
QY 361 EVCNDLENFTSGSPFLCNDLSYITALLXDGFGFADSTVLQLTKKVNNIETGALGATFHL 420
DB 361 EVCNDLENFTSGSPFLCNDLSYITALLXDGFGFADSTVLQLTKKVNNIETGALGATFHL 420
QY 421 LQSLGISH 428
DB 421 LQSLGISH 428
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Search completed: July 1, 2004, 13:50:11
Job time : 17.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 1, 2004, 13:42:31 ; Search time 10 Seconds
(without alignments)
2228.603 Million cell updates/sec

Title: US-10-091-085-7

Perfect score: 2252
Sequence: 1 MATSWGVTFVFLVYVSCVSA.....ETGVALGATFHLQLSLGISH 428

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2235	99.2	428	1 ENP5 HUMAN	O75356 homo sapien
2	1979.5	87.9	427	1 ENP5 MOUSE	Q9WU29 mus musculus
3	1918.5	85.2	469	1 ENP5 MESAU	Q9QY88 mesocricetu
4	996	44.2	484	1 ENP6 HUMAN	O75354 homo sapien
5	983	43.7	455	1 ENP6 RAT	O9ER31 rattus norv
6	488.5	21.7	518	1 GDAL YEAST	P32621 saccharomyc
7	484	21.5	455	1 NTPA_PEA	P52914 pisum sativ
8	441.5	19.6	454	1 APY_SOUTU	P80595 solanum tub
9	394	17.5	493	1 ENP1 CHICK	O93295 gallus gall
10	387	17.2	552	1 YBU4 CAEEL	Q21815 caenorhabdi
11	385	17.1	510	1 ENP1 MOUSE	P55772 mus musculus
12	382.5	17.0	485	1 YV4E CAEEL	O18411 caenorhabdi
13	375	16.7	513	1 ENP1 BOVIN	O18956 bos taurus
14	371	16.5	630	1 YNDT_YEAST	P40009 saccharomyc
15	367	16.3	510	1 ENP1 PIG	Q9MYU4 sus scrofa
16	366.5	16.3	613	1 ENP4 MOUSE	Q9DBT4 mus musculus
17	366	16.3	510	1 ENP1 HUMAN	P49961 homo sapien
18	363.5	16.1	511	1 ENP1 RAT	P97687 rattus norv
19	363	16.1	616	1 ENP4 HUMAN	O9Y237 homo sapien
20	357.5	15.9	529	1 ENP3 HUMAN	O75355 homo sapien
21	351.5	15.6	495	1 ENP2 MOUSE	O55026 mus musculus
22	321.5	14.3	495	1 ENP2 RAT	O35795 rattus norv
23	314.5	14.0	495	1 ENP2 CHICK	P79784 gallus gall
24	310.5	13.8	494	1 ENP2 BOVIN	O27893 toxoplasma
25	150	6.7	628	1 NTP1 TOXGO	O27895 toxoplasma
26	148	6.6	628	1 NTP2 TOXGO	P52913 toxoplasma
27	141	6.3	592	1 NTP4 TOXGO	P21333 spiroplasma
28	105.5	4.7	533	1 VGL_SPAV	O46796 streptococc
29	104.5	4.6	535	1 DEXB STRPN	Q34655 moxella th
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ALIGNMENTS

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RESULT 1
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AC O75356;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 5 precursor
DE (EC 3.6.1.6) (NTPDase5) (Nucleoside diphosphatase) (CD39 antigen-like
DE 4) (ER-UDPase).
GN NTPD5 OR CD39L4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Theria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leukemia;
RX MEDLINE=98341119; PubMed=9676430;
RA Chadwick B.P., Frischauf A.-M.;
RT "The CD39-like gene family: identification of three new human members
RT (CD39L2, CD39L3, and CD39L4), their murine homologues, and a member of
RT the gene family from Drosophila melanogaster.";
RL Genomics 50:357-367(1998).
CC -!- FUNCTION: Likely to promote reglycosylation reactions involved in
CC glycoproteins folding and quality control in the endoplasmic
CC reticulum. Hydrolyzes UDP, GDP AND IDP but not any other
CC nucleoside di-, mono- or triphosphates, nor thiamine pyrophosphate
CC (By similarity).
CC -!- CATALYTIC ACTIVITY: A nucleoside diphosphate + H(2)O = a
CC nucleotide + phosphate.
CC -!- COFACTOR: Requires calcium and magnesium.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
CC -!- TISSUE SPECIFICITY: Expressed in adult liver, kidney, prostate,
CC testis and colon. Much weaker expression in other tissues.
CC -!- SIMILARITY: Belongs to the GDAL / CD39 NTPase family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF039918; AAC39885.1; -.
CC Genew; HGNC:3367; ENTPD5.
CC MTM; 603162; -.
DR InterPro; IPR000407; GDAL_CD39_NTPase.
DR Pfam; PF01150; GDAL_CD39_1.
DR PROSITE; PS01238; GDAL_CD39_NTPASE; FALSE NEG.
KW Hydrolase; Transmembrane; Glycoprotein; Calcium; Magnesium;
KW Endoplasmic reticulum; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 428 ECTONUCLEOSIDE TRIPHOSPHATE
FT DIPIHOSPHOHYDROLASE 5.
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FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 368 368 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 428 AA; 47517 MW; 830437A155D24DDD CRC64;

Query Match 99.2%; Score 2235; DB 1; Length 428;
Best Local Similarity 99.3%; Pred. No. 1.2e-170;
Matches 425; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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D5 61 RIHVTVFVKQPGQPLILEGEVFDVSKPGLSAFVDQPKQAGTQVGLLEVAKDSIPRSHW 120
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D5 121 KKTPLVLCATAGLRLPEHAKALLFEVKEIFRSPFLVPKGSVIMTQDEGIFAWVTV 180
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D5 301 EPCYAEVLVRVGRKLHQPEEVQSGSYAFSYTYVAVDVTMDIDYKGGILKVEDFERKAR 360
QY 361 EVCNLENFTSGSPCLNDLVTALLXGDFGADSTVLQTKKVNINETGALGATPHL 420
D5 361 EVCNLENFTSGSPCLNDLVTALLXGDFGADSTVLQTKKVNINETGALGATPHL 420
QY 421 LQSLGISH 428
D5 421 LQSLGISH 428

RESULT 2
ID ENPS MOUSE STANDARD; PRT; 427 AA.
AC Q9WU29; O70214;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 5 precursor
DE (EC 3.6.1.6) (NTPDase5) (Nucleoside diphosphatase) (CD39 antigen-like
DE 4) (ER-UDPase).
GN ENTPD5 OR CD39L4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=98119025; PubMed=9457681;
RA Chadwick B.P., Williamson J., Sheer D., Frischaut A.-M.;
RT "CDNA cloning and chromosomal mapping of a mouse gene with homology to
RT NTPases.";
RL Mamm. Genome 9:162-164 (1998).
RN [2]
RP SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND CHARACTERIZATION.
RC TISSUE=Liver;
RX MEDLINE=99298181; PubMed=10369669;
RA Trombetta B.S., Helenius A.;
RT "Glycoprotein regucosylation and nucleotide sugar utilization in the
RT endoplasmic reticulum.";
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RL EMBO J. 18:3282-3292 (1999).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Komoto H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Kamanaka I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsch G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustinch S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaeerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Wushaw-Boris A., Yoshida K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Hayaishizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=FVB/N. TISSUE=Kidney;
MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Kulyk S.W.,
RA Villalón D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc Natl Acad Sci U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: Likely to promote regucosylation reactions involved in
CC glycoproteins folding and quality control in the endoplasmic
CC reticulum. Hydrolyzes UDP, GDP AND IDP but not any other
CC nucleoside di-, mono- or triphosphates, nor thiamine
CC pyrophosphate.
CC -!- CATALYTIC ACTIVITY: A nucleoside diphosphate + H(2)O = a
CC nucleotide + phosphate.
CC -!- COFACTOR: Requires calcium and magnesium.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- PTM: Glycosylated with high mannose N-linked glycans.
CC -!- MISCELLANEOUS: Optimal pH is neutral.
CC -!- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
DR EMBL; AF006482; AAC05181.1; -.
DR EMBL; AJ238636; CAB45533.1; -.
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DR EMBL; AK002618; BAB22234.1; --
DR EMBL; BC015247; AAH15247.1; --
DR MGI; 1321385; Entpds.
DR InterPro; IPR000407; GDAI_CD39_NTPase.
DR Pfam; PF01150; GDAI_CD39_1.
DR PROSITE; PS01238; GDAI_CD39_NTPase; FALSE NEG.
KW Hydrolase; Transmembrane; Glycoprotein; Calcium; Magnesium;
KW Endoplasmic reticulum; Signal.
FT SIGNAL 1 18
FT CHAIN 19 427
FT ECTONUCLEOSIDE TRIPHOSPHATE
FT DIPHOSPHOHYDROLASE 5.
FT CARBOHYD 41 41
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 231 231
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 390 390
FT CONFLICT 390 390
FT CONFLICT 394 427
FT PLTAKHSEKHROHMLGGLGHLSPAPVSGHGRPSSTSEAC
FT ISEPVFSQEVDSSETFSLGSKAWPETR {IN REF. 1}.
FT SQ SEQUENCE 427 AA; 47101 MW; 2P9DA2C342C55577 CRC64;

Query Match 87.9%; Score 1979.5; DB 1; Length 427;
Best Local Similarity 87.8%; Pred. No. 2.9e-150; Indels 1; Gaps 1;
Matches 3/4; Conservative 24; Mismatches 28;

QY 1 MATSWGTVPFVFLVWVSCVSAVSHRNQQTWPEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATSWGAV-FMLIIACVGVTVFYREQQTWPEGVFLSSMCPINVSAGTFYGINFDAGSTGT 59

QY 61 RIHVYTFVQKMPGQLPILGEVDFSVKPGLSAFVDPQKGAETVQGLLEVAKDSIPRSHW 120
DB 60 RIHVYTFVQKTAGLPFLEGEIFDSVKPGLSAFVDPQKGAETVQGLLEVAKDSIPRSHW 119

QY 121 KTPVVLKATAGLRLLPEHKAKALLFEVKIEFRKSPFLVPKGSVSMITQDEGIFAWVTV 180
DB 120 ERTPVVLKATAGLRLLPEKQAALLLEVEIEFRNSPFLVPGSVSMIDSGYEGILAWVTV 179

QY 181 NFLTQGLHGRQETVGTGLDGGASTQITFLPQFEKTLTPRPGYLTSPFNFSYTKLYTH 240
DB 180 NFLTQGLHGRQETVGTGLDGGASTQITFLPQFEKTLTPRPGYLTSPFNFSYTKLYTH 239

QY 241 SYLGFLGKAARLATALGALTEGTGHTFRSACLPRWLEAEWIFGVKGYQVGGNQEVEGF 300
DB 240 SYLGFLGKAARLATALGALTEGTGHTFRSACLPRWLEAEWIFGVKGYQVGGNQEVEGF 299

QY 301 EPCYAEVLVRVVKGLHQPVEVQSGSFYAFSYTYTDRVDTMDIYKGGILKVEDFERKAR 360
DB 300 EPCYAEVLVRVVKGLHQPVEVQSGSFYAFSYTYTDRVDTMDIYKGGILKVEDFERKAR 359

QY 361 EVCNDLENFTSGSPFLCMLSVITALLKDGFGPADSTVLQLTKKVNNIETGVALGATFHL 420
DB 360 EVCNDLGSFSSGSPFLCMLSVITALLKDGFGPADSTVLQLTKKVNNIETGVALGATFHL 419

QY 421 LQSLGIS 427
DB 420 LQSLGIT 426

RESULT 3
ENPS_MESAU
ID ENPS_MESAU STANDARD; PRT; 469 AA.
AC Q9QYC8; Q9QYC9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 5 precursor
DE (EC 3.6.1.6) (NTPDases) (Nucleoside diphosphatase) (CD39 antigen-like
DE 4) (ER-UDPase) (proto-oncogene cph).
GN ENTPD5 OR CD39L4 OR CPH.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=99142925; PubMed=9989819;
RA Velasco J.A., Avila M.A., Notario V.;
RT "The product of the cph oncogene is a truncated, nucleotide-binding
RT protein that enhances cellular survival to stress.";
RL Oncogene 18:689-701(1999).
CC !- FUNCTION: Likely to promote reglycosylation reactions involved in
CC glycoproteins folding and quality control in the endoplasmic
CC reticulum. Hydrolyzes UDP, GDP AND IDP but not any other
CC nucleoside di-, mono- or triphosphates, nor thiamine pyrophosphate
CC (By similarity).
CC !- CATALYTIC ACTIVITY: A nucleoside diphosphate + H(2)O = a
CC nucleotide + phosphate.
CC !- COFACTOR: Requires calcium and magnesium (By similarity).
CC !- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
CC !- TISSUE SPECIFICITY: Expressed in fetal cells and most adult
CC tissues.
CC !- DISEASE: Cph oncogene has transforming capacity and tumorigenic
CC potential.
CC !- SIMILARITY: Belongs to the GDAI / CD39 NTPase family.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF084568; AAF22931.1; ALT_TERM.
CC EMBL; AF084569; AAF22932.1; --
CC InterPro; IPR000407; GDAI_CD39_NTPase.
CC Pfam; PF01150; GDAI_CD39_1.
CC PROSITE; PS01238; GDAI_CD39_NTPase; FALSE NEG.
KW Hydrolase; Transmembrane; Glycoprotein; Calcium; Magnesium;
KW Endoplasmic reticulum; Signal; Proto-oncogene.
FT SIGNAL 1 18
FT CHAIN 19 469
FT ECTONUCLEOSIDE TRIPHOSPHATE
FT DIPHOSPHOHYDROLASE 5.
FT CARBOHYD 42 42
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SQ SEQUENCE 469 AA; 52125 MW; 03DBA23E0C73474B CRC64;

Query Match 85.2%; Score 1918.5; DB 1; Length 469;
Best Local Similarity 86.0%; Pred. No. 2.4e-145; Indels 3; Gaps 1;
Matches 361; Conservative 22; Mismatches 34;

QY 1 MATSWGTVPFVFLVWVSCVSAVSHRNQQTWPEGIFLSSMCPINVSASTLYGIMFDAGSTGT 60
DB 1 MATPWGAVFLLMIACAGSTVFYREQQTWPEGVFLSSMCPANVSASTFYGINFDAGSTGT 60

QY 61 RIHVYTFVQKMPGQLPILGEVDFSVKPGLSAFVDPQKGAETVQGLLEVAKDSIPRSHW 120
DB 61 RIHVYTFVQKAAAGLPFLEGEIFDSVKPGLSAFVDPQKGAETVQGLLEVAKDSIPRSHW 120

QY 121 KTPVVLKATAGLRLLPEHKAKALLFEVKIEFRKSPFLVPKGSVSMITQDEGIFAWVTV 180
DB 121 KTPVVLKATAGLRLLPEKQAALLLEVEIEFRKSPFLVDPDSVSMIDSGYEGILAWVTV 180

QY 181 NFLTQGLHGRQETVGTGLDGGASTQITFLPQFEKTLTPRPGYLTSPFNFSYTKLYTH 240
DB 181 NFLTQGLHGRQETVGTGLDGGASTQITFLPQFEKTLTPRPGYLTSPFNFSYTKLYTH 240

QY 241 SYLGFLGKAARLATALGALTEGTGHTFRSACLPRWLEAEWIFGVKGYQVGGNQEVEGF 300
DB 241 SYLGFLGKAARLATALGALTEGTGHTFRSACLPRWLEAEWIFGVKGYQVGGNQEVEGF 300

QY 301 EPCYAEVLVRVVKGLHQPVEVQSGSFYAFSYTYTDRVDTMDIYKGGILKVEDFERKAR 360
DB 301 EPCYAEVLVRVVKGLHQPVEVQSGSFYAFSYTYTDRVDTMDIYKGGILKVEDFERKAR 360

QY 361 EVCNDLENFTSGSPFLCMLSVITALLKDGFGPADSTVLQLTKKVNNIETGVALGATFHL 420
DB 361 EVCNDLENFTSGSPFLCMLSVITALLKDGFGPADSTVLQLTKKVNNIETGVALGATFHL 420

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361 EVCNDLESFTSGSPFLCMLDLSYITALLKDGFGFADGTLTLQTLTKKVNNIETQWPGG---HL 417

DB

ENP6_HUMAN
ID ENP6_HUMAN STANDARD; PRT; 484 AA.
AC O75354; Q90UD1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 6 (EC 3.6.1.6)
DE (NTPDase6) (CD39 antigen-like 2).
GN ENTPD6 OR CD39L2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Keratinocytes;
RX MEDLINE=98341119; PubMed=9676430;
RA Chadwick B.P., Frischauf A.-M.,
RT "The CD39-like gene family: identification of three new human members
RT (CD39L2, CD39L3, and CD39L4), their murine homologues, and a member of
RT the gene family from *Drosophila melanogaster*.";
RL Genomics 50:357-367(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Garder C., Carter N.P., Clee C.M.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A.G., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Leivaeslahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McKay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillipsmore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.B., Sehra H.K., Showkhen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas B.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.,
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -!- FUNCTION: Might support glycosylation reactions in the Golgi
CC apparatus and, when released from cells, might catalyze the
CC hydrolysis of extracellular nucleotides. Hydrolyzes preferentially
CC nucleoside 5'-diphosphates, nucleoside 5'-triphosphates are
CC hydrolyzed only to a minor extent, there is no hydrolysis of
CC nucleoside 5'-monophosphates. The order of activity with different
CC substrates is GDP > IDP > UDP = CDP > ADP (By similarity).
CC -!- CATALYTIC ACTIVITY: A nucleoside diphosphate + H(2)O = a
CC nucleotide + phosphate.
CC -!- COFACTOR: Requires calcium and magnesium (By similarity).
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. GOLGI. BUT ALSO
CC OCCURS IN A SOLUBLE EXTRACELLULAR FORM (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: Expressed in most tissues.
CC -!- SIMILARITY: Belongs to the GDAL / CD39 NTPase family.
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DR EMBL; AF039916; AAC39883.1; -;
DR EMBL; AL035252; CAB41571.1; -;
DR Genbank; HGNC:3368; ENTPD6.
DR MIM; 603160; -;
DR InterPro; IPR000407; GDAL_CD39_NTPase.
DR Pfam; PF01150; GDAL_CD39; -;
DR PROSITE; PS01238; GDAL_CD39_NTPase; FALSE NEG.
KW Hydrolyase; transmembrane; Glycoprotein; Calcium; Magnesium;
KW Signal-anchor; Golgi stack.
FT DOMAIN 1 39
FT TRANSMEM 40 60
FT CYTOPLASMIC (POTENTIAL).
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT LUMENAL (POTENTIAL).
FT N-LINKED (GLCNAC: .) (POTENTIAL).
FT CARBOHYD 220 220
FT CARBOHYD 284 284
FT CONFLICT 138 138
FT CONFLICT 202 202
FT CONFLICT 202 202
FT SEQUENCE 484 AA; 53233 MW; 27334B290B8D64C CRC64;
SQ
Query Match 44.2%; Score 996; DB 1; Length 484;
Best Local Similarity 52.4%; Pred. No. 8.5e-72;
Matches 204; Conservative 54; Mismatches 125; Indels 6; Gaps 4;
QY 40 PINVSA---STLYGIMFDAGSTGTRIHVYTFVQMPQGLFLEGEVDSVKPGLSAFVDQ 96
DB 90 PLGTAADGHEVFGIMEDAGSTGTRHVHFQFT-RPPRETPTLTHTFKAVKPGLSAADD 148
QY 97 PKQGAETVQGLLEVAKDSIPRSHWKTTPVVLKATAGLLPEHKAKALLPEVKIEPRKSP 156
DB 149 VKSAQGIREDLDVAKODIPDFPKATPLVKATAGLLPEGKAKLLQKVEVFKRASP 208
QY 157 FLVPKGSVSMTGDEGIFAWTVNFLTGLQHLGHQRTVCTLDLGASTQITFLPOFEKT 216
DB 209 FLVGDDCVSIMNGTDEGVSAWITNFLTGLSKTPGGSSVGMWLDLGGGSTQIAFLPRVEGT 268
QY 217 LEQTPRGILTSFEMFNSTYKLYTHSYLGRGLKARLITGLALETE-CTDGHTRFSAQLPR 275
DB 269 LQASPPGYLALRMFNFTYKLYSYLGLGMSARLAILGQVGEQPKAKGKELVSPCLSP 328
QY 276 WLEAFMTGGVKVQYQGNQGEVGEFPCYAEVLVRVVGKHLQHPVEEVQSGFYAFSYTYDR 335
DB 329 SPKGEHEAEVTVYVSGKAAASLHELCAARVSEVLQNRVHTEVKEVDFYAFSYTYDL 388
QY 336 AVDTDMIDYKGGILKVEDFERKARVCDNLENFTSGPFLCMDLSTYITALLKDGFGFAD 395
DB 389 AAGVGLDAEKGSLVVGDFEIAAKYVCRTLETQPOSSPFCMDLTYVSLQLQF-FGFPFR 447
QY 396 STVLQTLTKVNNIETGALGATPHLLQSL 424
DB 448 SKVLKLRKIDNVETSWALGAIFHYIDSL 476
RESULT 5
ENP6_RAT
ID ENP6_RAT STANDARD; PRT; 455 AA.
AC O9ER31.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 6 (EC 3.6.1.6)
DE (NTPDase6) (CD39 antigen-like 2).
GN ENTPD6 OR CD39L2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]

RT (aprase) from potato tubers (Solanum tuberosum).";
RL Biochem. Biophys. Res. Commun. 218:916-923(1996).
RN [2]
RP SEQUENCE OF 42-54; 68-95 AND 236-253.
RC STRAIN: cv. Désirée;
RA MEDLINE=9635615; PubMed=8703025;
RX Vasconcelos E.G., Ferreira S.T., de Carvalho T.M.U., de Souza W.,
Ketellun A.M., Mancilla M., Valenzuela M.A., Verjovsky-Almeida S.;
RT "Partial purification and immunohistochemical localization of ATP
diphosphohydrolase from Schistosoma mansoni. Immunological cross-
reactivities with potato apyrase and Toxoplasma gondii nucleoside
triphosphate hydrolase.";
RL J. Biol. Chem. 271:22139-22145(1996).
CC -!- FUNCTION: Catalyzes the hydrolysis of phosphoanhydride bonds of
nucleoside tri- and di-phosphates.
CC -!- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
CC -!- COFACTOR: Calcium.
CC -!- SUBCELLULAR LOCATION: Membrane-associated (Probable).
CC -!- PTM: The N-terminus is blocked.
CC -!- SIMILARITY: Belongs to the GDAL / CD39 NTPase family.
CC -----
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DR EMBL; U58597; AAB02720.1; -;
DR PIR; JC4616;
DR InterPro; IPR000407; GDAL_CD39_NTPase.
DR Pfam; PF01150; GDAL_CD39; 1; NTPASE; 1.
DR PROSITE; PS01238; GDAL_CD39_NTPASE; 1.
KW Hydrolase; Transmembrane; Calcium; Signal.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 454 APYRASE.
FT TRANSMEM 426 446 POTENTIAL.
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 454 AA; 50041 MW; 9D9FE431DAF52F CRC64;

Query Match 19.6%; Score 441.5; DB 1; Length 454;
Best Local Similarity 28.6%; Pred. No. 1.2e-27;
Matches 130; Conservative 78; Mismatches 178; Indels 69; Gaps 16;

Qy 25 NQQTFFGIFLS-----SMCPINVS-----STLIGMFDAGSTGRHYV 65
Db 3 NQNGHPIFILAIFLVPLSLSKNVAQIPLRHLLSHSEHYAVIFDAGSTGRVHF 62

Qy 66 TFVQKMPQLPILSG-EVFDVSKPLGSAFVDPQKGAETVGLLEVAKDSIPRSHWKTIP 124
Db 63 RFDEKL-GLLPIGNNIEYFMAEPGLSYAEDPKAANSLEPLDGAEGVVPQLQSETP 121

Qy 125 VVKATGRLRLPEHKAVALFEVKEIFR-KSPFLVPKGSVSIWQDEGIFAWTVNVL 183
Db 122 LELGATAGRLKGADEAKILQAVRNLYPNQSTFHSKDQWVTLDTGTCESYMAAATNYL 181

Qy 184 TGLHGHROETVGTLDLGGASTQTTEL---POPEKTILE-OTPRGYLTSFEMFNSTYKLT 239
Db 182 LGNLGDKYKSTAIIDLOGSSVQVAYALSIEQPAKAPQNEDEGFYVQOKHLMKDYNLV 241

Qy 240 HSYLGFGLKAARLATLGALETGTDTGHTFRSACLPRWLEAEWIFGGYKYQVGNQGEV 299
Db 242 HSYLNGQLAGRAIFKASRNES-----NPCALEGCDGYSYGGVYKVPKPGS-- 292

Qy 300 FEPYAEVLRVRG--KLHQPEEVQVGSF-----YAFSYVYDRAVDMDI 342
Db 293 ----SWKFCRRLTRHALKLNKCNIECTFNGVMNGGDDGQKXNHASSFFYDGAQGV 349

Qy 343 DYE-KGGILKYVEDPERKAREVCD-NLENFTS-----GSPFLCMLDSLVIALLKDGFG 392
Db 350 DTKFPSALAKPIQVYLNAAKACQTNVADIKSIFPKTQDRNIPVLCMDLIYEYTLVDGFG 409

Qy 393 F---ADSTVLQLRKKVNN-IETGWLCAQTEPHLQS 423
Db 410 LNPHEKITVHDVQYKYNLVGAAMPGLGCAIDLVSS 444

RESULT 9
ID ENPI_CHICK STANDARD; PRT; 493 AA.
AC O93295;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2003 (Rel. 42, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE (NTPDase1) [Ecto-ATP diphosphohydrolase] (ATPase) (lymphoid cell
DE activation antigen) (Ecto-apyrase) (CD39 antigen).
GN ENTPD1 or CD39.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-21 AND 150-156.
RC TISSUE=Oviduct.
RX MEDLINE=98298108; PubMed=9632655;
RA Nagy A.K., Knowles A.F., Nagami G.T.;
RT "Molecular cloning of the chicken oviduct ecto-APP-
diphosphohydrolase.";
RL J. Biol. Chem. 273:16043-16049(1998).
RN [2]
RP SEQUENCE OF 1-17.
RC TISSUE=Stomach;
RX MEDLINE=97442428; PubMed=9295305;
RA Lewis-Carl S., Kirley T.L.;
RT "Immunolocalization of the ecto-ATPase and ecto-apyrase in chicken
RT gizzard and stomach. Purification and N-terminal sequence of the
RT stomach ecto-apyrase.";
RL J. Biol. Chem. 272:23645-23652(1997).
CC -!- FUNCTION: In the nervous system, could hydrolyze ATP and other
CC nucleotides to regulate purinergic neurotransmission. Could also
CC be implicated in the prevention of platelet aggregation.
CC Hydrolyzes ATP and ADP equally well (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
CC -!- COFACTOR: Requires calcium and magnesium (By similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (Probable).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the GDAL / CD39 NTPase family.
CC -----
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the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF041355; AAC26491.1; -;
DR InterPro; IPR000407; GDAL_CD39_NTPase.
DR Pfam; PF01150; GDAL_CD39; 1.
DR PROSITE; PS01238; GDAL_CD39_NTPASE; 1.
KW Hydrolase; Transmembrane; Antigen; Glycoprotein; Calcium; Magnesium.
FT DOMAIN 1 7 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 8 28 POTENTIAL.
FT DOMAIN 29 463 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 464 486 POTENTIAL.
FT DOMAIN 487 493 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 65 65 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL; AF005940; AAB62382.1; -- NTPase.
DR InterPro; IPR000407; GDAI_CD39_NTPase.
DR Pfam; PF01150; GDAI_CD39_1.
DR PROSITE; PS01238; GDAI_CD39_NTPase; 1.
KW Hydrolase; Transmembrane; Antigen; Glycoprotein; Calcium; Magnesium.
FT DOMAIN 1 16
FT TRANSMEM 17 37
FT DOMAIN 38 481
FT TRANSMEM 482 502
FT DOMAIN 503 513
FT CARBOHYD 73 73
FT CARBOHYD 227 227
FT CARBOHYD 245 245
FT CARBOHYD 307 307
FT CARBOHYD 336 336
FT CARBOHYD 373 373
FT CARBOHYD 460 460
FT CONFLICT 97 97
FT CONFLICT 101 103
FT CONFLICT 464 464
SQ SEQUENCE 513 AA; 58113 MW; 20FE98F27B6D2F96 CRC64;
Query Match 16.7%; Score 375; DB 1; Length 513;
Best Local Similarity 26.7%; Pred. No. 2.9e-22;
Matches 130; Conservative 72; Mismatches 177; Indels 108; Gaps 19;
QY 8 VFFMLVVCVCSAVSHRNQQTWFEGLFLLSCMCPINVSASTLYGIMPDAGSTGRIHVYTF 67
DB 17 ILSILGFSCTIAVIA-----LLALGTONKALPENK-----FGLVLDAGSSHTSLIYRW 67
QY 68 VQKMPGQLPILGEVEFDSVK-PGLSAFVDPQKQAEVQGLLEVAKDSIPRSEKKTTPVV 126
DB 68 PAEKENDTVVQIEBSNVKPGISGPAKNEINVLTACMERAKQVIPSIGHMETPVY 127
QY 127 LKATAGRLI-PEHK-AKALLPEVKIPEKSPPLVPKSGVIMTQDEGIPAWVTYNFL 183
DB 128 LGATAGMELLRMENKQADKILAAVASSISEYFF--DFQCARISGQERAGYGHITVNYL 185
QY 184 TQGL-----HGHQETVGTLDGASTQITFLPQFEKTLBOTPRGYLTSPEMF 231
DB 186 LKKTQKLSWFLKPSKDDTQETVGLDGLGASTQITFVFNQNTT--ESPNNL-YFRLY 242
QY 232 NSTYKLYTHSYLGFGLKARLATLGALETGTG-----V 265
DB 243 GKYSVYTHSFLCYGKQALLQKL-ALGLQGTNGIHEPCFHSRYMKIKMSVLNESPCT 301
QY 266 --HTFRSACLPRMLEAEWIFGQVKYQYGGNQEVEGFEPCVAVYLRV-----V 311
DB 302 KRHEINLSFYP-----LVDIIRGAGN-----FQCRQSIQLPNTSYCPYSSCSF 347
QY 312 RGKLHQPEEVQSGFYAFSYVYDRAVDTMDIDYKGGILKVEDFERKAREVC----- 363
DB 348 NGVFLPLHGFQGAFAFYV-----MEFLNLTSESVSEVQLEKTELEFCAQRWEVQ 401
QY 364 ---DNLENFTSGSPFLCMDLSYITALLKDGFGF-ADS-TVLQUTKKVNNIETGWLGA 417
DB 402 KNFGEVKEKLYSE---YCFSGTYILVLLNGYHFTASSKNHIFWKNRSDVCGTTLGYM 458
QY 418 FHLQLSL 424
DB 459 LNLTKNI 465
RESULT 14
YNDI YEAST
ID YNDI YEAST
AC P40009;
DT 01-FEB-1995 (Rel. 31, Created)
PRT; 630 AA.
STANDARD;
QY 103 TVQGLLEVAKDSIPRSHKKTTPVVLKATAGRLILPEHKAVALPEVKEIPEKSPFL-VPK 161
DB 84 YLTFLRFAEEHIEYEQIGETDILLIFATAGMLLPEAQKDAIKNGLQNGKSVTALRVSD 143
QY 162 GSVIMTQGDIGIFAWVTNPLTQGLGHROETVGTLDLGGASTQITFLPQFEK----- 215
DB 144 SNIRLIDGAWESIYSWAVNVLGFRDKENDSKYGMIDMGASVQIAFELANEKESYNGG 203
QY 216 TLEQTPGRLTSEFMNSYTKLYTHSYLGFGLKARLATLGALETGTGHTFASACLPR 275
DB 204 NVYSINLGSITENEDYK--YKIYSTFLGYGANGLKKYENSELVKSGNS-----NDSCSPR 257
QY 276 WLBAEWIFGQVKYQYGGNQEVEGFEPCVAVYLRVVRGKLHQPE----- 319
DB 258 GLNR--LIQ-----RFTVNGTGE--WDVCLAQVSSLI-GDKAQPSCPNPTCFLRNVIAPSV 308
QY 320 EVQSGSFYAFS-YYVDRAVDTMDIDYKGGILKVEDFERKAREVC-----DNLENFTSGSP 374
DB 309 NLSTVQLYGFSEYVYTTIS-----NFGSGGBYHYQKFTDEVRYCKQKMDNDIQDGFKRNE 362
QY 375 F-----LCMDLSYITALLKDGFGFADST--VLQLTKKVANNIETGWLGA----- 416
DB 363 FPNADIERLGNCFKAAWVTSLVHDGFN-VDTKHLFOSVLKIAEEMQNALGAMLYHSK 421
QY 417 ---TTHLQSLGIS 427
DB 422 DLKENLLSOLEVA 434
RESULT 13
ENPI BOVIN
ID ENPI BOVIN
AC O18956;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE [NTPase] (Ecto-ATP diphosphohydrolase) (ATPase) (lymphoid cell
DE activation antigen) (CD39 antigen) (Ecto-apyrase).
GN ENTPD1 OR CD39.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN
RX SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RC MEDLINE=97115858; PubMed=8955160;
RX Kaczmarek E., Koziak K., Seivigny J., Siegel J.B., Anrather J.,
RA Beaudoin A.R., Bach P.H., Robson S.C.;
RT Identification and characterization of CD39/vascular ATP
RT diphosphohydrolase.;
RL J. Biol. Chem. 271:33116-33122(1996).
CC -!- FUNCTION: In the nervous system, could hydrolyze ATP and other
CC nucleotides to regulate purinergic neurotransmission. Could also
CC be implicated in the prevention of platelet aggregation.
CC Hydrolyzes ATP and ADP equally well.
CC -!- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
CC -!- COFACTOR: Requires calcium and magnesium.
CC -!- SUBUNIT: Homodimer; disulfide-linked (5y similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the GDAI / CD39 NTPase family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Golgi apyrase (EC 3.6.1.5) (ATP-diphosphatase) (Adenosine
DE diphosphatase) (ADPase) (ATP-diphosphohydrolase) (Golgi nucleoside
DE diphosphatase)
GN YND1 OR YER005M
OS Saccharomyces cerevisiae (Baker's yeast)
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RN SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=S288C;
RC STRAIN=93340091; PubMed=10409709;
RX Gao X.D., Kaigrodov V., Jigami Y.,
RA "YND1, a homologue of GDA1, encodes membrane-bound apyrase required
RT for Golgi N- and O-glycosylation in Saccharomyces cerevisiae";
RL J. Biol. Chem. 274:21450-21456(1999).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RC MEDLINE=97313264; PubMed=9169868;
RA Dietrich F.S., Mulligan J.R., Hennessy K.M., Yelton M.A., Allen E.,
RA Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E.,
RA Cherry J.M., Chung E., Durcan M., Guzman E., Hartzell G.,
RA Hunick-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari D., Lew H.,
RA Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P.,
RA Oh C., Petel P.X., Roberts D., Sehl P., Schramm S., Shogren T.,
RA Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome V";
RL Nature 387:78-81(1997).
CC -1- FUNCTION: Catalyzes the hydrolysis of phosphoanhydride bonds of
CC nucleoside tri- and di-phosphates. Has equal high activity toward
CC ADP/ATP, GDP/GTP, and UDP/UTP and approximately 50% less toward
CC CDP/CTP and thiamine pyrophosphate. Has no activity toward GMP.
CC Required for Golgi glycosylation and cell wall integrity.
CC -1- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
CC -1- PATHWAY: Glycosylation.
CC -1- SUBCELLULAR LOCATION: Golgi; membrane-bound.
CC -1- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; AF203695; AAP17573.1; --
DR EMBL; U18778; AAB64538.1; --
DR PIR; S50463; S50463.
DR GenOnline; 139085; --
DR SGD; S0000807; YND1.
DR GO; GO:001710; P:nucleoside diphosphatase activity; IDA.
DR GO; GO:0006486; P:protein amino acid glycosylation; IMP.
DR InterPro; IPR000407; GDA1_CD39_NTPase.
DR Pfam; PF01150; GDA1_CD39; 1.
DR PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
KW Hydrolase; Transmembrane; Golgi stack.
FT DOMAIN 1 500 LUMENAL (POTENTIAL).
FT TRANSMEM 501 517 POTENTIAL.
FT DOMAIN 518 630 CYTOPLASMIC (POTENTIAL).
FT SEQUENCE 630 AA; 71851 MW; 02P8D24A78212544 CRC64;
Query Match 16.5%; Score 371; DB 1; Length 630;
Best Local Similarity 26.0%; Pred. No. 8.1e-22;
Matches 116; Conservative 75; Mismatches 164; Indels 92; Gaps 17;
49 YGIMFDAGSTGRTHVYTF-----VQMPQQLPILSGE---VFDVKPGLSA 92
10 FGIVIDAGSGSRIRHVFVKQDTESLLHATNQDSQILQSVPHIQEKDWTF-KLNPGLSS 68

QY 93 FVDQKQGAET-VQGLLEKVAKDSIPRSHWKTPPVVLKATAGLRLLPEHAKALLPEV-KE 150
DB 69 FKKQDQAYKSHIKELLPKNNILPESHWSGCPVFIQATAGNLLPQDIQSSILDLGCG 128
QY 151 IFRKSPFLVP--KGSVSMTGQDEGIFAWTVNFTLQGLHGRQE-----TVGTLDLGA 203
DB 129 LKHPAEFLVEDCSAQIQVIDGETGLYGLGLNLYLYGHFNDFYNPEVSDHFTFGFMDWGA 188
QY 204 STQIIFLPQFETLE-----QTPRGVLTSPFMENSTYKLYTHSYLGFGLKAARL 252
DB 189 STQIAFAPHDSGEIAHRDDIATIFLRSVNGDLQKWDVFVST-----WLGFGANQARR 241
QY 253 ATLGAL-----ETEGTDGHTFRSACLPRLWEAEWIFGGVYVYGGNQEGEVGFE 301
DB 242 RYLAQLINTLPENTNDYENDDFSTRNLNDPCMPRGSSDTDFEKTDTIFHAGSNGYBQCTK 301
QY 302 PCVAEVLK-----VVRGKLGHOPE-EVQRSGSFYAFSVYDRAVDTMDIVKKGGLKV 352
DB 302 STYPLLLKNMPCDDEPCLFNGVHAPRIDPANKFICTSEYTWANDV-----FKLGSEYNF 357
QY 353 EDPFKAREVCQN-----LENFTSG-----SPFL---CMDSYITALLKDGFGPA--- 394
DB 358 DKFSKSLREFCSNWTQILANSKGVVNSIPENFLKDACFKGNWVNLILHEGDFMDRIDV 417
QY 395 -----DSTVHLQTKKNNIETGALG 415
DB 418 DAENVNDRPLFQSVKVEKRELSWTILG 444
RESULT 15
ENPL_PIG STANDARD; PRT; 510 AA.
AC Q9MYU4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
DE (NTPase) (Ecto-ATP diphosphohydrolase) (ATPase) (Lymphoid cell
DE activation antigen) (Ecto-apyrase) (CD39 antigen).
OS ENTPI1 OR CD39.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Aortic endothelium;
RX MEDLINE=20325090; PubMed=10866813;
RA Lemmens R., Vanduffel L., Kittel A., Beaudoin A.R., Benrezzak O.,
RA Sevigny J.;
RA "Distribution, cloning, and characterization of porcine nucleoside
RT triphosphate diphosphohydrolase-1";
RL Eur. J. Biochem. 267:4106-4114(2000).
RN [2]
RN SEQUENCE OF 202-220.
RC TISSUE=Pancreas;
RX MEDLINE=97115858; PubMed=8955160;
RA Kaczmarek E., Kozlak X., Sevigny J., Siegel J.B., Anrather J.,
RA Beaudoin A.R., Bach P.H., Robson S.C.;
RT "Identification and characterization of CD39/vascular ATP
RT diphosphohydrolase";
RL J. Biol. Chem. 271:33116-33122(1996).
CC -1- FUNCTION: In the nervous system, could hydrolyze ATP and other
CC nucleotides to regulate purinergic neurotransmission. Could also
CC be implicated in the prevention of platelet aggregation.
CC Hydrolyzes ATP and ADP equally well.
CC -1- CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.
CC -1- COFACTOR: Requires calcium and magnesium (by similarity).
CC -1- SUBUNIT: Homodimer; disulfide-linked (by similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: Highest expression found in vascular
CC endothelium, smooth muscle, spleen and lung.
CC -1- PTM: CLEAVED IN TWO POLYPEPTIDES THAT SEEM TO STAY TOGETHER BY

